

GenCore version 4.5  
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OM nucleic - nucleic search, using sw model

Run on: October 3, 2001, 18:10:06 ; Search time 134.89 Seconds  
(without alignments)  
8378.849 Million cell updates/sec

Title: US-09-532-263-4

Perfect score: 1800

Sequence: 1 TCTACAGCCTTACCCACT.....TTCCTGGAGATTACTACG 1800

Scoring table:

IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 730101 seqs, 313950809 residues

Total number of hits satisfying chosen parameters: 1460202

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : N\_Geneseq\_0601.\*

- 1: /SID88/gcgdata/geneseq/geneseq/NA1980.DAT.\*
- 2: /SID88/gcgdata/geneseq/geneseq/NA1981.DAT.\*
- 3: /SID88/gcgdata/geneseq/geneseq/NA1982.DAT.\*
- 4: /SID88/gcgdata/geneseq/geneseq/NA1983.DAT.\*
- 5: /SID88/gcgdata/geneseq/geneseq/NA1984.DAT.\*
- 6: /SID88/gcgdata/geneseq/geneseq/NA1985.DAT.\*
- 7: /SID88/gcgdata/geneseq/geneseq/NA1986.DAT.\*
- 8: /SID88/gcgdata/geneseq/geneseq/NA1987.DAT.\*
- 9: /SID88/gcgdata/geneseq/geneseq/NA1988.DAT.\*
- 10: /SID88/gcgdata/geneseq/geneseq/NA1989.DAT.\*
- 11: /SID88/gcgdata/geneseq/geneseq/NA1990.DAT.\*
- 12: /SID88/gcgdata/geneseq/geneseq/NA1991.DAT.\*
- 13: /SID88/gcgdata/geneseq/geneseq/NA1992.DAT.\*
- 14: /SID88/gcgdata/geneseq/geneseq/NA1993.DAT.\*
- 15: /SID88/gcgdata/geneseq/geneseq/NA1994.DAT.\*
- 16: /SID88/gcgdata/geneseq/geneseq/NA1995.DAT.\*
- 17: /SID88/gcgdata/geneseq/geneseq/NA1996.DAT.\*
- 18: /SID88/gcgdata/geneseq/geneseq/NA1997.DAT.\*
- 19: /SID88/gcgdata/geneseq/geneseq/NA1998.DAT.\*
- 20: /SID88/gcgdata/geneseq/geneseq/NA1999.DAT.\*
- 21: /SID88/gcgdata/geneseq/geneseq/NA2000.DAT.\*
- 22: /SID88/gcgdata/geneseq/geneseq/NA2001.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1800	100.0	1800	17 AAT17869	Human interleukin-
2	1746.2	97.0	2456	17 AAT33278	Human interleukin-
3	1638.6	91.0	1682	21 AAF20958	Human low adenodin
4	1638.6	91.0	1682	21 AAF21320	Human low adenodin
5	1638.6	91.0	1682	21 AAA34836	Human adenosine re
6	1638.6	91.0	1682	21 AAA35198	Human adenosine re
7	1638.6	91.0	3791	21 AAF20960	Human low adenodin
8	1638.6	91.0	3791	21 AAF21322	Human low adenodin
9	1638.6	91.0	3791	21 AAA34838	Human adenosine re
10	1638.6	91.0	3791	21 AAA35200	Human adenosine re
11	1549.2	86.1	1696	21 AAF20957	Human low adenodin

12	1549.2	86.1	1696	21	AAF21319	Human low adenodin
13	1549.2	86.1	1696	21	AAA34835	Human adenosine re
14	1549.2	86.1	1696	21	AAA35197	Human adenosine re
15	976.4	54.2	1705	17	AAT17868	Murine interleukin
16	954.2	53.0	1714	17	AAT32613	Murine Etl-2 gene.
17	783.6	43.5	1140	21	AAZ40400	Murine soluble int
18	284.2	15.8	296	16	AAT21651	Human gene signatu
19	87	4.8	413	21	AAF20959	Human low adenodin
20	87	4.8	413	21	AAF21321	Human low adenodin
21	87	4.8	413	21	AAA34837	Human adenosine re
22	87	4.8	413	21	AAA35199	Human adenosine re
23	49	2.7	975	21	AAA70701	Human interleukin
24	49	2.7	1035	21	AAZ40288	SR345 coding seque
25	49	2.7	1074	18	AAV04440	Interleukin 6 rece
26	49	2.7	1260	20	AAZ09202	Human IL-6 recepto
27	49	2.7	1486	19	AAV60296	Human interleukin-
28	49	2.7	1545	21	AAA70763	IL-6R/IL-6 fusion
29	49	2.7	1627	18	AAT97848	Human fusion polyp
30	49	2.7	2061	10	AAAN90340	Sequence encoding
31	49	2.7	2066	14	AAQ41746	IL-6 receptor codi
32	49	2.7	2087	10	AAAN90847	DNA contg. region
33	49	2.7	3319	17	AAT31441	Interleukin-6 rece
34	49	2.7	3319	19	AAV60295	Human interleukin-
35	49	2.7	3319	21	AAF21364	Human low adenodin
36	49	2.7	3319	21	AAA35242	Human adenosine re
37	49	2.7	3507	21	AAA09046	Fusion polypeptide
38	49	2.7	4513	21	AAF21365	Human low adenodin
39	49	2.7	4873	21	AAA35243	Human adenosine re
40	47.8	2.7	3477	21	AAA09047	Fusion polypeptide
41	46.2	2.6	1363	19	AAV42919	Truncated Interleu
42	46.2	2.6	1369	19	AAV42918	Truncated Interleu
43	46.2	2.6	2541	12	AAQ13113	DNA encoding IL-6
44	46.2	2.6	2542	13	AAQ24235	IL-6R for soluble
45	44.6	2.5	20674	21	AAC58017	Arachidonic acid m

#### ALIGNMENTS

RESULT 1  
AAT17869 standard; DNA; 1800 BP.  
ID AAT17869 standard; DNA; 1800 BP.  
AC AAT17869;  
XX  
XX  
DT 21-MAY-1996 (first entry)  
XX  
DE Human interleukin-11 receptor alpha chain gene.  
XX  
KW Haemopoietin; interleukin-11; IL-11; receptor; agonist; antagonist;  
KW therapy; diagnosis; ss.  
XX  
XX Homo sapiens.  
XX  
FH Key  
CDS Location/Qualifiers  
FT 108..1399  
FT /\*tag= a  
FT sig\_peptide 108..196  
FT /\*tag= b  
FT mat\_peptide 197..1396  
FT /\*tag= c  
XX  
XX WO9607737-A1.  
XX  
XX 14-MAR-1996.  
XX  
XX 05-SEP-1995; 95WO-AU00578.  
XX  
XX 05-SEP-1994; 94AU-0007902.  
XX  
XX 05-SEP-1994; 94AU-0007901.  
XX  
XX (AMRA-) AMRAD OPERATIONS PTY LTD.  
XX



RESULT	2	
AAT33278		
ID	AAT33278 standard; cDNA; 2456 BP.	
XX	AAT33278;	
XX		
XX	09-OCT-1996 (first entry)	
XX		
XX	Human interleukin-11 receptor cDNA.	
DE		
XX	Interleukin-11 receptor; IL-11 receptor; antibody; antagonist; bone;	
KW	osteoporosis; Paget disease; myeloma; ds.	
KW		
OS	Homo sapiens.	
XX		
XX	Key	Location/Qualifiers
FT	CDS	734..2002
FT		/*tag= a
FT	sig_peptide	734..802
FT		/*tag= b
FT	mat_peptide	803..1999
FT		/*tag= c
FT		
PN	W09619574-A1.	
XX		
XX	27-JUN-1996.	
PD		
XX		
XX	27-NOV-1995;	95WO-US15400.
PF		
XX		
XX	22-DEC-1994;	94US-0362304.
PR		
XX		
XX	(GEMV ) GENETICS INST INC.	
PA		
XX		
PI	Tobin JF;	
XX		
XX	WPI; 1996-309588/31.	
DR	P-PSDB; AAR99090.	
DR		
XX		
PT	New nucleic acid encoding human interleukin 11 receptor - and	
PT	related protein, antibodies, receptor antagonists, etc, useful for	
PT	treating and preventing loss of bone mass	
XX		
XX	Claim 1; Page 31-34; 54pp; English.	
XX		
CC	A cDNA clone (AAT33278) codes for human interleukin-11 (IL-11)	
CC	receptor (AAR99090), a protein that may play a role in the regulation	
CC	of bone maturation and repair. The cDNA clone, designated PHILIR14-	
CC	2, was isolated from a human activated peripheral blood mononuclear	
CC	cell cDNA library in ZAPII using probes derived from the murine EtL-	
CC	2 gene (see also AAT32613). This sequence, or fragments of it (pref.	
CC	nts 803-1828, 1907-1999, 734-1999, 1067-1828 or 1067-1999), can be	
CC	expressed in host systems and the recombinant protein used to treat	
CC	diseases associated with loss of bone mass or to raise antibodies.	
XX		
XX	Sequence 2456 BP; 487 A; 679 C; 773 G; 517 T; 0 other;	
XX		
Query Match	97.0%;	Score 1746.2; DB 17; Length 2456;
Best Local Similarity	99.0%;	Pred. No. 0;
Matches 1794; Conservative	0; Mismatches	3; Indels 16; Gaps
QY	1	TCTAACAGCCTTACCCCACTTGGTCATCAATTTTCTCCTAGGAAGCCTCAGTTTGGG 60
Db	606	tctaacagccttaccacacttggtgatcaattttctcctctaggaagcctcagtttggg 665
QY	61	GAGGAGAGCCAGGCTTTAG-CATCCATCTCAGGGGTGCGGGATTTTTCGACTCTACCTCT 119
Db	666	gaggaaagacaggcttagctcccatctcaggggtcggggatttttgactctacctct 725
QY	120	CCCCACAGATGACACGAGCTGCTCAGGCTGAGCAGGCTCCTGCTGGCCGCTGCCTACAG 179
Db	726	ccccacagaTgagcagcagctgctcagggctgagcagggctctggtggcgtgggtcacag 785



Db 364 gccaagcagccgactatgagaactctcttgcaacttgagtcgccagcagatcagcggtt 423  
 QY 546 TACCCACCCGCTACCTACCTCTACAGGAAGAAGACAGTCCCTAGGAGCTGATAGCCAGA 605  
 Db 424 taccacccgctaccctaccctcctacaggaagaagacagtcctcagagcctgatagcacga 483  
 QY 606 GGAGGAGTCCATCACAGGCGCCCTGCGCCATGCCACAGGATCCCTAGGGGCTGCCCGCT 665  
 Db 484 ggaagagtcacatcacagggccctggccatgccacagagatccctagggctggccgct 543  
 QY 666 GTGTTGTCACGGGGCTGAGTTCGTGAGCCAGTACCGGATTAATGACAGTGAAGTGAACC 725  
 Db 544 gtgtttccacggggtgagttctgagccagtcaccggattaatgtaactgactgaggtgaacc 603  
 QY 726 CACTGGTGTGTCACACAGCGCTGCTGGATGTGAGCTGTGACAGCATCTTCGCGCCCTG 785  
 Db 604 cactg---9gtgcagacacgctgctggtgagtcgagtcgagacatctctgcccctg 660  
 QY 786 ACCACCCAGGCGCTGCGGGTAGTCACTACAGGTTACCCCGAGGCGCTCGAGCCCA 845  
 Db 661 accacccagggcctgaggtagagtcagtcacaggttaccccccagcgcctgagacca 720  
 QY 846 GCTGGACATACCTGCTGCTGCGCGTGCAGCCGCCACCTTCCTGCTCAAGTTCGGTTGC 905  
 Db 721 gctggacataacctgctcctgctgcccgtgcagcccaacttctctgcaagttccgtttgc 780  
 QY 906 AGTACCGTCCGGCGGACAGTCCACGCTGTGTCACGCTGGAGCCAGCTGGAGGAGG 965  
 Db 781 agtacgctccgcccagatcccaagcctgttccacgctggagccagctggaactggaag 840  
 QY 966 TGATCAGAGTGTGGGTGGGCTGCCCATGCTGCTGAGTCACTGAGTCACTGAGTTC 1025  
 Db 841 tgatcacagatgctggctgggctgcccacatgctgacagtcagtgccgggacttc 900  
 QY 1026 TAGATGCTGGCACCTGGAGCACCTGGAGCCCGAGGCGCTGGGGAATCCGAGCACATGGGA 1085  
 Db 901 tagatgctggcacctggagcacctggagcccgaggcctgggaaactccgagcactggga 960  
 QY 1086 CCATACCAAGGAGATACAGCATGGGCGCAGCTACACAGCCAGCAGGTTGGAGCCTC 1145  
 Db 961 ccatacaagaagataccagcagtgaggccagctacacagcagccagaggtggagccctc 1020  
 QY 1146 AGTGACAGCCCTGCTCTCCCAAGGCCCTCCCTCCCAACACACCCCTCGCTACTTGTATC 1205  
 Db 1021 agtggacagcctgctcctccaaggccctccctccacacacacccctcggtacttgatc 1080  
 QY 1206 ACAGGACTCTGTGGAGCAGTACGTGCTGCTGGCGTCTTGGGAATCCTTTCTTCTG 1265  
 Db 1081 acaggactctgtggagcaggtagctgtgctggcgtcttgggaatcccttcttctctg 1140  
 QY 1266 GACTGTGGCTGGGGCCCTGGCACTGGGCTCTGGCTGAGGCTGAGCAGGGGTGGGAAGG 1325  
 Db 1141 gactggctggcctggcctggcctggcctggcctggcctggcctggcctggcctggcct 1200  
 QY 1326 ATGGATCCCAAGACCTGGGTTCTTGGCCCTCAGTGTATTCAGTGGACAGCGCTCCAGGAG 1385  
 Db 1201 atgatatcccaagcctgggttcttggcctcagtgatccagtggaacagcgtccagag 1260  
 QY 1386 CTCCAACCTGTAGAGACCCAGGAGGCTTGGGAGATTCACCTATATTCCTGTCTTG 1445  
 Db 1261 ctccaacactgtagaggacccagagggcttcggcagattccaccctataattctgtctg 1320  
 QY 1446 CTGGTGTGATAGAACACAGGAGGACAGTATGATCCCTATGGTTGGATCTCAGCTGGAG 1505  
 Db 1321 ctggctgtgataagaacccagcagcagtagatccctatggctgacatccagctggaag 1380  
 QY 1506 TCTGTTGGAGCCCATTTCTGTGAGACCTGTATTTCAAAATTTGAGCTGAAAGGTGCT 1565  
 Db 1381 ttctgtttgagccattctgtgagaccctgtatttcaaatgttcagctgaaaggtgct 1440  
 QY 1566 TGTACTCTGATTTTACCCCGAGGTTGGAGTTCCTGCTCAAGGAACGTGTATGTGTAC 1625

Db 1441 tctacctgtatttcccccagagtggtgtctgtccaaggaacgtgtgtaattgttac 1500  
 QY 1626 ATCTGTCTCATCTGTACCATGTGTGTGAAGCAGGGGACATGTATTCTCTGCATGCA 1685  
 Db 1501 atctgtctccatgtgaccatgtctgtgagcaggggaacatgtattctctgcgtgca 1560  
 QY 1686 TGTATGTAGTGTGCTGGGAGTGTGTGGTCTCTTGGCTCTTGGCCCTTTCCCTTCGAG 1745  
 Db 1561 tgtatgtaggctgggagtggtggtgctctggctctggccttt--ccttgacag 1618  
 QY 1746 GGTTTGTGAGTGTGAATAAAGAGATAAGGAAGTCTTGGAGATTAATCTCAG 1800  
 Db 1619 gggttgtgaggtgtgaataaagaagaaggaagttcttggagattatactcag 1673

RESULT 4  
 AAF21320  
 ID AAF21320 standard; DNA; 1682 BP.  
 XX  
 AC AAF21320;  
 XX  
 DT 14-MAR-2001 (first entry)  
 XX  
 DE Human low adenosine antisense oligonucleotide related sequence #2887.  
 KW Low adenosine antisense oligonucleotide; phosphorothioate; allergy;  
 KW human; airway disorder; bronchoconstriction; lung inflammation;  
 KW surfactant depletion; respiratory; bronchodilator; antiinflammatory;  
 KW immunosuppressive; antiasthmatic; anesthetic; hypotensive; cytostatic;  
 KW respiratory obstruction; pulmonary obstruction; impeded respiration;  
 KW surfactant hypoproduction; pulmonary vasoconstriction; asthma; RDS;  
 KW respiratory distress syndrome; pain; cystic fibrosis; allergic rhinitis;  
 KW pulmonary hypertension; emphysema; pulmonary transplantation rejection;  
 KW chronic obstructive pulmonary disease; pulmonary infection; bronchitis;  
 KW cancer; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200062736-A2.  
 XX  
 PD 26-OCT-2000.  
 XX  
 PF 24-MAR-2000; 2000WO-US08020.  
 XX  
 PR 06-APR-1999; 99US-0127958.  
 XX  
 PA (UYEC-) UNIV EAST CAROLINA.  
 PA (NYCE/) NYCE J W.  
 XX  
 PI Nyce JW;  
 XX  
 XX WPI; 2000-679539/66.  
 DR  
 XX  
 PT Low adenosine (A) content antisense oligonucleotides which do not  
 PT trigger adenosine receptors during metabolism, useful e.g. for treating  
 PT cancers and respiratory obstructions -  
 XX  
 PS Disclosure; Page 1324-1325; 1592pp; English.  
 XX  
 CC The present invention describes low adenosine (A) content antisense  
 CC oligonucleotides and compositions (I) comprising them. In the antisense  
 CC oligonucleotides the A is replaced by a 'Universal' or alternative base.  
 CC (I) can have respiratory, bronchodilator, antiinflammatory, analgesic,  
 CC immunosuppressive, antiasthmatic, hypotensive and cytostatic activities.  
 CC The antisense oligonucleotides and (I) can be used to down-regulate the  
 CC expression and or activity of target polypeptides associated with  
 CC lung/respiratory disorders and malignancies, such as stimulating and  
 CC activating peptide factors and transmitters, transcription factors,  
 CC immunoglobulins and antibodies, antibody receptors, cytokines and  
 CC chemokines, endogenously produced specific and non-specific enzymes,  
 CC binding proteins, adhesion molecules and their receptors, cytokine and  
 CC chemokine receptors, adenosine receptors, bradykinin receptors, central  
 CC nervous system (CNS) and peripheral nervous and non-nervous system



KW Human; adenosine receptor; low adenosine antisense oligonucleotide;  
 KW phosphothioate; impaired respiration; inflammation; allergy;  
 KW allergic disease; bronchoconstriction; inhibitor; antiinflammatory;  
 KW antiallergic; antiasthmatic; cytotatic; analgesic; impaired airway;  
 KW lung disease; ischaemic condition; pulmonary vasoconstriction; asthma;  
 KW respiratory distress syndrome; pain; cystic fibrosis; emphysema;  
 KW pulmonary hypertension; chronic obstructive pulmonary disease; COPD;  
 KW cancer; leukaemia; lymphoma; carcinoma; metastasis; ss.  
 \*XX Homo sapiens.  
 XX WO200009525-A2.  
 PN 24-FEB-2000.  
 PD 03-AUG-1999; 99WO-US17712.  
 XX 03-AUG-1998; 98US-0095212.  
 PR (UYEC-) UNIV EAST CAROLINA.  
 PA NYce JW;  
 PI WPI; 2000-205971/18.  
 XX New antisense oligonucleotides useful for treating e.g. pulmonary  
 PT vasoconstriction, inflammation, allergies, asthma, hypertension,  
 PT bronchitis, emphysema, respiratory distress syndrome, ischemia or  
 PT cancers -  
 XX Disclosure; Page 691-692; 1343pp; English.  
 XX The present invention describes a new composition comprising an  
 CC antisense oligonucleotide (ON) with low adenosine (up to 15%), which  
 CC targets nucleic acids involved in bronchoconstriction, allergies, and/or  
 CC inflammation. The ON can have antiinflammatory, antiallergic,  
 CC antiasthmatic, cytotatic and analgesic activities. The compositions are  
 CC useful for the treatment of diseases associated with inflammation,  
 CC impaired airways, including lung disease and diseases whose secondary  
 CC effects afflict the lungs of a subject. They can be used for treating  
 CC e.g. ischaemic conditions, pulmonary vasoconstriction, allergies,  
 CC asthma, impaired respiration, respiratory distress syndrome, pain, cystic  
 CC fibrosis, pulmonary hypertension, emphysema, chronic obstructive  
 CC pulmonary disease (COPD), and cancers such as leukemias, lymphomas,  
 CC carcinomas, and cancers which may metastasize to the lungs, including  
 CC breast and prostate cancer. The reduction of the adenosine content of  
 CC the ONs reduces side effects. The A-containing ONs break down with the  
 CC release of deoxyadenosine which activates adenosine receptors causing  
 CC bronchoconstriction and inflammation. AAA32313 to AAA35312 represent  
 CC nucleotide sequences given in the sequence listing from the present  
 CC invention, which correspond to SEQ ID NO:1 to 2815, and then the last  
 CC 185 sequences are also called SEQ ID NO:1 to 185, but the sequences  
 CC differ from the previously named sequences. SEQ ID NO:11 to 1680  
 CC (AAA32323 to AAA33992) are specifically claimed ONs from the present  
 CC invention. N.B. Sequences given in the disclosure of the present  
 CC invention do not match up with their corresponding SEQ ID NO: sequences  
 CC given in the sequence listing.  
 XX  
 XX Sequence 1682 BP; 324 A; 476 C; 521 G; 361 T; 0 other;

Query Match 91.0%; Score 1638.6; DB 21; Length 1682;  
 Best Local Similarity 99.5%; Pred. No. 0;  
 Matches 1666; Conservative 0; Mismatches 4; Indels 5; Gaps 2;

QY 126 AGATGACAGAGCTGCTCAGGGCTGACAGGGGTCCTGGGCGCTGACAGCCCTGG 185  
 Db 4 agatgacagcagctgctcagggctgacagggctcctggtggcgtgctacagccctgg 63  
 QY 186 TGTCTGCTCTCTCCCTGCCCCAGGCTGGGCCCCCCCCAGGGGTCCTGATGGGAGC 245  
 Db 64 tgtctgctctctctccctgccccagggcctggggccccccagggggtccagtatgggcagc 123

QY 246 CAGCAGGTCCTCGTGAAGCTGTGTGCTCTGAGTACTGCCGGGACCCAGTGTCTCTGGT 305  
 Db 124 caggcaggtccgtgaagctgtgtgtctctgagtgactgctgcggggaccacagtgctctggt 183  
 QY 306 TTCCGGATGGGGAGCCAAAGCTGCTCCAGGACCTGACCTCTGGCTAGGCGATCACTGG 365  
 Db 184 ttcggatggggagccaaagctgctccaggagctgactctggctggctagggcatgaactgg 243  
 QY 366 TCTGTGCCCCAGGACAGACACTGATGAGGACCTACATCTGCCAGACCTCTGATGGTGG 425  
 Db 244 tctgtgcccaggcagacagcactgatgagggcaacctacatctgccagaccctgagtggtg 303  
 QY 426 CACTTGGGGCACAGTACACCTGCAGCTGGGCTACCTCCAGCCCGCCCTGTGTCTCTCT 485  
 Db 304 cacttggggcacagtacacctgagctgggtacacctccagcccgccctgttgtctcct 363  
 QY 486 GCCAAGCAGCCGACTATGAGAACTTCTTGCACCTTGGAGTCCAGCCAGCTCAGCGGTT 545  
 Db 364 gccaaagcagccgactatgagaactctcttgcaactggagctccagccagcagatcagcggtt 423  
 QY 546 TACCACCCCGCTACCTCACCTCTACAGGAAGACAGTCTCTAGGAGCTGATAGCCAGA 605  
 Db 424 taccaccgctacctcaacctctacaggaagaagacagtccttagagctgatagccaga 483  
 QY 606 GGAGGAGTCCATCCACAGGCCCCCTGCCATGCCACAGGATCCCTTAGGGGCTGCCCGCT 665  
 Db 484 ggagagtgccatccacagggccctggccatgccacagatccctctagggctgcccgt 543  
 QY 666 GTGTTGTCACGGGGCTGAGTTCTGGAGCCAGTACCCGGATTATGTGACTGAGGTGAACC 725  
 Db 544 gtgtgtccacggggctgagttcttgagccagtagccggttaattgactgaggtgaacc 603  
 QY 726 CACTTGGTGTGTCAGCACACGCTGCTGGATGTGAGCTTGCAGAGCATCTTTCGCCCTG 785  
 Db 604 cactg---ggctgcagcacacgctgctggtgagcttgagagacatctgcgcctg 660  
 QY 786 ACCACCCCCAGGGCCTGCGGGTAGAGTACAGGATACCCCGAGGCTCGCGAGCCA 845  
 Db 661 accacccccaggcctgctgggtgagtcagtagtaccaggtaccctccgacgctcgagcca 720  
 QY 846 GCTGGACATACCTGCTCTCTGGCGTGCAGCCCGACCTTCTCTGCTCAAGTTCGTTTGC 905  
 Db 721 gctggacataacctgctcctgctgctggcgtgccagccccacttctgctcaagttcctgtgc 780  
 QY 906 AGTACCTGTCGCGCGCAGCATCCAGCCTGTGTCAGGGTGAGCCAGCTGGAGTGGAGGAGG 965  
 Db 781 agtacctccgctgcagcatcccgcttgcacagcggcagctggagctggagggaggg 840  
 QY 966 TGATCAGAGATGCTGTGGCTGGGCTGCCCATGCTGTACAGTACAGTCCCGGGGACTTTC 1025  
 Db 841 tgatcacagatgctgtgctggctgctgccccatgctgtacgagtcagtgccgggacttc 900  
 QY 1026 TAGATGTGACCTGAGGACCTGAGCCCGGAGGCTGGGAACTCCGAGGACTGGGA 1085  
 Db 901 tagatgctgcacgtgagcacctggagcccgaggcctgggaaactccagagcactggga 960  
 QY 1086 CCATACCAAGAGAGATACACAGCATGGGGCCAGCTTACACAGCAGCCAGAGTGGAGGCTC 1145  
 Db 961 ccataccaaaggagataccagcagctggggcagctacacagcagcagagggagagctc 1020  
 QY 1146 AGGTGGAGACCCCTGCTCTCCAGAGCCCTCCCTCCCAACACACACCTCGGCTACTTGATC 1205  
 Db 1021 aggtggacagccctgctctcccaaggccctccctcccaacacacacccctcggtactgtatc 1080  
 QY 1206 ACAGGGAATCTGTGGACAGGTAGCTGTGCTGGGCTCTTTGGGAATCCTTCTTCTCTGG 1265  
 Db 1081 acagggaactctgtgagcaggtagctgtgctggcgtctttggggaatcctcttctctcgtg 1140  
 QY 1266 GACTGTGGCTGGGGCCCTGGCACTGGGGCTTCTGGCTGAGGCTCAGAGCGGGTGGGAAGG 1325  
 Db 1141 gactggctggctggggccctggcagctggggcctggcagctggagctggagacggggggaggg 1200  
 QY 1326 ATGGATCCCCAAAGCCTGGGTTCTTGGCCCTCAGTGTATTCAGTCCAGAGCGCTCCAGGAG 1385















[illegible]

RESULT 10  
AAA35200  
ID AAA35200 standard; DNA; 3791 BP.  
XX  
XX AAA35200;  
XX  
DT 28-JUL-2000 (first entry)

Human adenosine receptor related polynucleotide 2nd SEQ ID NO:74.

Human; adenosine receptor; low adenosine antisense oligonucleotide; phosphorothioate; impaired respiration; inflammation; allergy; allergic disease; bronchoconstriction; inhibitor; antiinflammatory; antiallergic; antiasthmatic; cytostatic; analgesic; impaired airway; lung disease; ischaemic condition; pulmonary vasoconstriction; asthma; respiratory distress syndrome; pain; cystic fibrosis; emphysema; pulmonary hypertension; chronic obstructive pulmonary disease; COPD; cancer; leukaemia; lymphoma; carcinoma; metastasis; ss.

Homo sapiens.

WO200009525-A2.

24-FEB-2000.

03-AUG-1999; 99WO-US17712.

03-AUG-1998; 98US-0095212.

(UYEC-) UNIV EAST CAROLINA.

Nyce JW;

WTI; 2000-205971/18.

New antisense oligonucleotides useful for treating e.g. pulmonary vasoconstriction, inflammation, allergies, asthma, hypertension, bronchitis, emphysema, respiratory distress syndrome, Ischemia or cancers

Disclosure; Page 1241-1242; 1343pp; English.

The present invention describes a new composition comprising an antisense oligonucleotide (ON) with low adenosine (up to 15%), which targets nucleic acids involved in bronchoconstriction, allergies, and/or inflammation. The ON can have antiinflammatory, antiallergic, antiasthmatic, cytostatic and analgesic activities. The compositions are useful for the treatment of diseases associated with inflammation, impaired airways, including lung disease and diseases whose secondary effects afflict the lungs of a subject. They can be used for treating e.g. ischaemic conditions, pulmonary vasoconstriction, allergies, asthma, impeded respiration, respiratory distress syndrome, pain, cystic fibrosis, pulmonary hypertension, emphysema, chronic obstructive pulmonary disease (COPD), and cancers such as leukaemias, lymphomas, carcinomas, and cancers which may metastasize to the lungs, including breast and prostate cancer. The reduction of the adenosine content of the ONs reduces side effects. The A-containing ONs break down with the release of deoxyadenosine which activates adenosine receptors causing bronchoconstriction and inflammation. AAA32313 to AAA35312 represent the nucleotide sequences given in the sequence listing from the present invention, which correspond to SEQ ID NO:1 to 2815, and then the last 185 sequences are also called SEQ ID NO:1 to 185, but the sequences differ from the previously named sequences. SEQ ID NO:11 to 1680 (AAA32323 to AAA33992) are specifically claimed ONs from the present invention. N.B. Sequences given in the disclosure of the present invention do not match up with their corresponding SEQ ID NO: sequences given in the sequence listing.

Sequence 3791 BP: 716 A; 1087 C; 1151 G; 837 T; 0 other:

	Query Match	91.08;	Score 1638.6;	DB 21;	Length 3791;
	Best Local Similarity	99.5%;	Pred. No. 0;		
	Matches 1666;	Conservative	0;	Mismatches	4; Indels 5; Gaps 2;
QY	126	AGATGAGCAGCAGTGTCTAGGGCTGACGAGGGTCTGGTGGCGTGCGCTACAGCCCTGG	185		
Db	1700	agatgacgacgagtgtctcagggtgtcaggggttcctgggtggccgtggctacagccctgg	1759		
QY	186	TGTCGTGCTCTCTCCCTCGTGCCTCCAGCCCTGGGSCCTCCAGGGGTCTCAGTATGGGCAGC	245		

Db	1760	 tgctgctccctccctgccccagagctggggccccccaggggtccagtatgggcagc	1819
QY	246	CAGCGAGGTCCGTGAAGCTGTGTCTCTGGAGTCACTGCCGGGACCACAGTGCCTGGT	305
Db	1820	caggcaagtcctgtaagctgtgtctctggagtgaactgcgaggagcccaagtgcctcgtt	1879
QY	306	TTCGGGATGGGAGGCCAAAGCTGCTCCAGGGACCTGACTCTGGGCTAGGGCATGAATGG	365
Db	1880	ttcgggatgggagccaaagctgtccagggaacctgactctgggctagggcgatgaactgg	1939
QY	366	TCCTGGCCAGGACAGACACACTGATGATGAGGGACACTACATCTGCCAGACCTGATGGT	425
Db	1940	tcctggcccaaggacagacactgatgaggccactacatctgcacacccctggatgggtg	1999
QY	426	CACCTTGGGGCACAGTGACCCCTGCAGCTGGGTACCCCTCCAGCCCGCCCTTGTCTCTCT	485
Db	2000	cacttggggcacagtgaacctgcagctgggtacctaccctccagccgacctgtgtctcct	2059
QY	486	GCCAAAGCCGACNATGAGAACTTCTTGCACCTTGAGATCCCGACCCAGATCAAGCGGTT	545
Db	2060	gccaaagccagactatgaaactctctgcaactggatgcccagagatccctcagccagtcagc	2119
QY	546	TACCCACCCGGCTACCTCACTCCTCTACAGGAAGACAGTCTCTAGGAGCTCATACCCAGA	605
Db	2120	taccaccgcctacctcactcctcagagaagacagtcctcaggagctgatagccaga	2179
QY	606	GGAGGAGTCCATCCACAGGGCCCTGGCCATGCCACAGGATCCCTTAGGGGCTCCCGCT	665
Db	2180	ggaggagtccatccacagggccctggccatgcccacagatccctcaggggctccgcct	2239
QY	666	GTGTGTCCACGGGGCTGAGTTCTGGAGCCAGTACCGGATTAAATGTGACTCAGGTGAACC	725
Db	2240	gttgttccacgggctgagttctggagccagtcaccgattaaatgtgactgagtgaaacc	2299
QY	726	CACTGGGTGTGCCACACACGCGCTGCTGGATGTGAGCTTGCAGAGCATCTTGGCCCTG	785
Db	2300	cactg---ggtgcagacacgctgctggatgtgagcttcgagagcatcttgcgcctg	2356
QY	786	ACCCACCCAGGGCCTGGGGTAGTCACTACCAAGTTACCCCGAGGCTCGCAGGCCA	845
Db	2357	accaccccaaggcttgcgggtagagtaagtaaccaggttaccccgacgacctgcagcca	2416
QY	846	GCTGGACATACCTGCTCCTCGCCGTGCCAGCCCACTTCTCTGCTCAAGTTCGTTTGC	905
Db	2417	gctggacataccctgctcttgcgctgcagccccaactctctgctcaagttcgtttgc	2476
QY	906	AGTACCGTCCGGGACAGTCCAGCTGCTGTCACCGTGGAGCCAGCTGAGCTGGAGAGG	965
Db	2477	agtaccgtccggcgagcatccagctggctcacgggtggccagctggaactggagaggtg	2536
QY	966	TGATCACAGATGCTGTGGCTGGGCTGCCCACTGCTGTACGAGTCAAGTCCCGGACTTTC	1025
Db	2537	tgatcacagatgtgtggctgggctggccatgtgtacgagtcagtgcccggagcttc	2596
QY	1026	TAGATGCTGGCACCCTGGAGCACCCTGGAGCCCGAGGCTGGGGAATCCCGAGCTGGGA	1085
Db	2597	tagatctggcaacctggagcaactggagccggagggctgggaactccgagcactggga	2656
QY	1086	CCATACCAAGAGATACCAAGATGGGGCCAGCTACACAGCAGCAGAGGTGGAGGCTC	1145
Db	2657	ccataccaaagagataccacgatggggccagctacacagcagccagagtggaacctc	2716
QY	1146	AGGTGACAGCCCTGCTCTCCAGGCCCTCCTCCACACACACCTCGGCTACTTGATC	1205
Db	2717	agggtgacagccctgctctccaaggccctccctccaaccacacccctcgctacttgatc	2776
QY	1206	ACAGGACTCTGTGGAGCAGGTAGCTGTGCTGGCGTCTTTGGGAATCTTTTCTCTGG	1265
Db	2777	acagggactctgtggagcaggtagctgtgtcggcgctcttgggaatcccttcttctcctg	2836
QY	1266	GACTGTGTGGTGGGGCCCTGGCACTTGGGCTCTGGCTGAGGCTGAGACGGGGTGGGAGG	1325

Db	2837	gactggtggtggtgggcccgtggaactggggctctggctgaagcgtgagcggggtgggaagg	2896
Qy	1326	ATGATCCCAAAAGCCTGGGTCTTGGCCCTCAGCTGATTCACGTGACAGGGCTGCAGGAG	1385
Db	2897	atgatcccaaacgctgggtctctggcctcagtgatccagtgacagcgctccagag	2956
Qy	1386	CTCAAACCTGTAGAGACCCAGAGGGCTTGGCAGATTCCACCTATTAATCCTGTCTTG	1445
Db	2957	ctccaaacctgtagagaccagagggcttcggcagattccaccataaattctgtcttg	3016
Qy	1446	CTGTGTGTGGATAGAAACCGACGACAGTAGATCCCTATGCTTGGATCTCAGCTGGAAG	1505
Db	3017	ctggtgtggtatagaaacccagcgcaagtagatccctatggtttgagatcctcagctggag	3076
Qy	1506	TTCGTTTGGAGCCCAPTTCTGTGAGACCCCTGTATTTCAAATTTGCAGCTGAAAAGTGCT	1565
Db	3077	tctgtttggagcccaattctgtgagaccctgtatttccaaatttcagctgaaaagtgct	3136
Qy	1566	TGTACCTCTGATTTCAACCCAGAGTTGGAGTCTGCTCAAGCAACGTCGTAAATGCTGAC	1625
Db	3137	tctacctctgatttccaccagagtttggaagttctgctcgaagaaagctgtgaaagtgtcac	3196
Qy	1626	ATCTGTGTCCATGTGTGACCATGTGCTGTGAAGACCCCTGTATTTCTCTGTCATGCA	1685
Db	3197	atctgtgtccatggtgaccatgtctgtgagcagggagacatgtattctctgcatgca	3256
Qy	1686	TGTATGTAGTGCCCTGGGAGTCTGTGTGGTCCTTGGCTCTTGGCCCTTCCCTCTGCAG	1745
Db	3257	tgtatgcagtgacctggggagtggtgtgtgggtcccttggtctctggccctt--ccttgca	3314
Qy	1746	GGTGTGTGCAGGTGTGAATAAAGAGAAATAAGGAAGTCTCTTGAGATTTACTCTAG	1800
Db	3315	gggttggcaggtgtaataaagagaataaggaagttcttgagattactcag	3369
RESULT 11			
ID	AAF20957 standard; DNA; 1696 BP.		
XX			
AC	AAF20957;		
XX			
DT	14-MAR-2001 (first entry)		
XX			
DE	Human low adenosine antisense oligonucleotide related sequence #2524.		
XX			
KW	Low adenosine antisense oligonucleotide; phosphorothioate; allergy;		
KW	human; airway disorder; bronchoconstriction; lung inflammation;		
KW	surfactant depletion; respiratory; bronchodilator; antiinflammatory;		
KW	immunosuppressive; antiasthmatic; analgesic; hypotensive; cytostatic;		
KW	respiratory obstruction; pulmonary obstruction; impeded respiration;		
KW	surfactant hypoproduction; pulmonary vasoconstriction; asthma; RDS;		
KW	respiratory distress syndrome; pain; cystic fibrosis; allergic rhinitis;		
KW	pulmonary hypertension; emphysema; pulmonary transplantation rejection		
KW	chronic obstructive pulmonary disease; pulmonary infection; bronchitis;		
KW	cancer; ss.		
XX			
OS	Homo sapiens.		
XX			
PN	WO200062736-A2.		
XX			
PD	26-OCT-2000.		
XX			
PF	24-MAR-2000; 2000WO-US08020.		
XX			
PR	06-APR-1999; 99US-0127958.		
XX			
PA	(UYEC-) UNIV EAST CAROLINA.		
PA	(NYCE/) NYCE J W.		
XX			
PI	Nyce JW;		
XX			
DR	WPI; 2000-679539/66.		
XX			







QY	961	GGAGGTGATCACAGATGCTGTGGCTGGGCTGCCCATGCTGTACGAGTCACTGCCCGGGA	1020
Db	989		
Db	892	ggagggtgatacagatagtctgtggctgggctgccccatgctgtaogatcagtgcccgggga	951
QY	1021	CTTTCTAGATGTGGCACCTTGAGCACCCTGGAGCCGAGGCGCTGGGGAACCTCCGAGCAC	1080
Db	952	ctttctagatgctggacactggagcactggagccggagcctggggaactccgagcac	1011
QY	1081	TGGGACCATACAAAGGAGATACCAGTATGGGGCCAGCTACACACGACGACGAGGTGGA	1140
Db	1012	tgggaccataccaagagataccagcatggggcagctacacacgagccagaggtggga	1071
QY	1141	GCCTCAGGTGGACAGCCCTGCTCCCAAGGCGCTCCCTCAACACACACCTCGGCTACT	1200
Db	1072	ggctccagggtggacagccctgtctctccaaaggccctccctcaacacacacctggctact	1131
QY	1201	TGATCACAGGGACTCTGTGGACAGGTAGCTGTGCTGGCGCTCTTTGGGAATCCTCTCTTT	1260
Db	1132	tgatacagggactctgtgagcaggtagctgtgctggctcttgggaaactccttcttt	1191
QY	1261	CTTGGGACTGGTGGGCGCCCTGGCACTGGGCGCTGTGGCTGAGGCTGAGACGGGGTGG	1320
Db	1192	ctctgggacctgggtggggccctggcactgggctctggctggagctggaacgggggtgg	1251
QY	1321	GAAGGATGGATCCCAAGCCCTTGGCGCTCAGTGATTCCAGTGACGACAGGCGTCC	1380
Db	1252	gaaggatgatacccaaggctggcttctggcctcagtgattccagtggaacggcgctcc	1311
QY	1381	AGAGCTCCAACTGTAGAGGACCCAGAGGGCTTGGCGAGATTCACCTATAATCCTG	1440
Db	1312	aggagctccaaacctgtagagaccagagggtctggcgagattccacctataactctg	1371
QY	1441	TCCTTGCTGTGGATAGAAACAGCGAGGACAGTAGATCCCTATGTTGGATCTCAAGT	1500
Db	1372	tccttgctgtgtgatagaacacaggagacagtagataccctatggttgagatcagct	1431
QY	1501	GGAGTTCGTTTGGAGCCCATTTCTGTGAGACCTGTATTTCAAAATTTGCAGCTGAAG	1560
Db	1432	ggaagttctgttggagccattctctgtagaccctgtatttcaaatlttgcagctggaag	1491
QY	1561	GTGCTGTACTCTGATTTTACCCACAGAGTTGGAGTTCCTGCTCAAGGAACGTGTGAATG	1620
Db	1492	gtgctgtacctctgattcaaccacagagtggagttctgtctcaaggaaacgtgtgtaagt	1551
QY	1621	TGTACATCTGTGCCATGTGTGACCATGTGCTGTGAAG--CAGGGAACATGTATT--CTC	1677
Db	1552	tgtacatctgttccatgtgtgaccatgtgtctgtggaaggccagggaaacatgattctctc	1611
QY	1678	TGATGCACTGATGTAGGTGCGCTGGGGAGTGTGTGGGTCCTTGGCTCTTGCGCTTTTC	1737
Db	1612	tgatgcatgatagtgaagggtcctgg---gagtggtgtgtgtgtccctgtctgtggccctctcc	1668
QY	1738	CTTGCAGGGGTTGTGCAGGTGTGAATAA	1767
Db	1669	c---ttacagagtttgscaggtatgaataaa	1696

RESULT 13

RESULT:  
AAA34835

AAA34833  
ID AAA34835 standard: DNA: 1696 bp.

XX  
ID  
AAA.

AC AAA:

XX  
XX

DT 28-3

XX

DE  
Huma

XX

KW Human

KW photo:

respiratory distress syndrome; pain; cystic fibrosis; emphysema;  
pulmonary hypertension; chronic obstructive pulmonary disease; COPD;  
cancer; leukaemia; lymphoma; carcinoma; metastasis; ss.

Homo sapiens.

WO200009525-A2.

24-FEB-2000.

03-AUG-1999; 99WO-US17712.

03-AUG-1998; 98US-0095212.

(UYEC-) UNIV EAST CAROLINA.

Nyce JW;

WPI; 2000-205971/18.

New antisense oligonucleotides useful for treating e.g. pulmonary  
vasoconstriction, inflammation, allergies, asthma, hypertension,  
bronchitis, emphysema, respiratory distress syndrome, ischemia or  
cancers -

Disclosure; Page 691; 1343pp; English.

The present invention describes a new composition comprising an  
antisense oligonucleotide (ON) with low adenosine (up to 15%), which  
targets nucleic acids involved in bronchoconstriction, allergies, and/or  
inflammation. The ON can have antiinflammatory, antiallergic,  
antiasthmatic, cytostatic and analgesic activities. The compositions are  
useful for the treatment of diseases associated with inflammation,  
impaired airways, including lung disease and diseases whose secondary  
effects afflict the lungs of a subject. They can be used for treating  
e.g. ischemic conditions, pulmonary vasoconstriction, allergies,  
asthma, impeded respiration, respiratory distress syndrome, pain, cystic  
fibrosis, pulmonary hypertension, emphysema, chronic obstructive  
pulmonary disease (COPD), and cancers such as leukaemias, lymphomas,  
carcinomas, and cancers which may metastasize to the lungs, including  
breast and prostate cancer. The reduction of the adenosine content of  
the ONs reduces side effects. The A-containing ONs break down with the  
release of deoxyadenosine which activates adenosine receptors causing the  
bronchoconstriction and inflammation. AAA32313 to AAA35312 represent the  
nucleotide sequences given in the sequence listing from the present  
invention, which correspond to SEQ ID NO:1 to 2815, and then the last  
185 sequences are also called SEQ ID NO:1 to 185, but the sequences  
differ from the previously named sequences. SEQ ID NO:11 to 1680  
(AAA32323 to AAA33992) are specifically claimed ONs from the present  
invention. N.B. Sequences given in the disclosure of the present  
invention do not match up with their corresponding SEQ ID NO: sequences  
given in the sequence listing.

Sequence 1696 BP; 315 A; 488 C; 529 G; 364 T; 0 other;

Query Match 86.1%; Score 1549.2; DB 21; Length 1696;  
Best Local Similarity 98.2%; Pred. No. 0;  
Matches 1621; Conservative 0; Mismatches 18; Indels 11; Gaps 5;

121 CCCACAGATGAGCAGCAGCTGCTCAGGGCTGAGCAGGGTCTGGTGGCCGTACAGC 180

[illegible]

b 55 caccqaatgaqcaqcaqctqctcaqgqctgaqcaqgqctcctqgtqgcccqgtqgctacagc 114

2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30 31 32 33 34 35 36 37 38 39 40 41 42 43 44 45 46 47 48 49 50 51 52 53 54 55 56 57 58 59 60 61 62 63 64 65 66 67 68 69 70 71 72 73 74 75 76 77 78 79 80 81 82 83 84 85 86 87 88 89 90 91 92 93 94 95 96 97 98 99 100 101 102 103 104 105 106 107 108 109 110 111 112 113 114 115 116 117 118 119 120 121 122 123 124 125 126 127 128 129 130 131 132 133 134 135 136 137 138 139 140 141 142 143 144 145 146 147 148 149 150 151 152 153 154 155 156 157 158 159 160 161 162 163 164 165 166 167 168 169 170 171 172 173 174 175 176 177 178 179 180 181 182 183 184 185 186 187 188 189 190 191 192 193 194 195 196 197 198 199 200 201 202 203 204 205 206 207 208 209 210 211 212 213 214 215 216 217 218 219 220 221 222 223 224 225 226 227 228 229 230 231 232 233 234 235 236 237 238 239 240 241 242 243 244 245 246 247 248 249 250 251 252 253 254 255 256 257 258 259 260 261 262 263 264 265 266 267 268 269 270 271 272 273 274 275 276 277 278 279 280 281 282 283 284 285 286 287 288 289 290 291 292 293 294 295 296 297 298 299 300 301 302 303 304 305 306 307 308 309 310 311 312 313 314 315 316 317 318 319 320 321 322 323 324 325 326 327 328 329 330 331 332 333 334 335 336 337 338 339 340 341 342 343 344 345 346 347 348 349 350 351 352 353 354 355 356 357 358 359 360 361 362 363 364 365 366 367 368 369 370 371 372 373 374 375 376 377 378 379 380 381 382 383 384 385 386 387 388 389 390 391 392 393 394 395 396 397 398 399 400 401 402 403 404 405 406 407 408 409 410 411 412 413 414 415 416 417 418 419 420 421 422 423 424 425 426 427 428 429 430 431 432 433 434 435 436 437 438 439 440 441 442 443 444 445 446 447 448 449 450 451 452 453 454 455 456 457 458 459 460 461 462 463 464 465 466 467 468 469 470 471 472 473 474 475 476 477 478 479 480 481 482 483 484 485 486 487 488 489 490 491 492 493 494 495 496 497 498 499 500 501 502 503 504 505 506 507 508 509 510 511 512 513 514 515 516 517 518 519 520 521 522 523 524 525 526 527 528 529 530 531 532 533 534 535 536 537 538 539 540 541 542 543 544 545 546 547 548 549 550 551 552 553 554 555 556 557 558 559 560 561 562 563 564 565 566 567 568 569 570 571 572 573 574 575 576 577 578 579 580 581 582 583 584 585 586 587 588 589 590 591 592 593 594 595 596 597 598 599 600 601 602 603 604 605 606 607 608 609 610 611 612 613 614 615 616 617 618 619 620 621 622 623 624 625 626 627 628 629 630 631 632 633 634 635 636 637 638 639 640 641 642 643 644 645 646 647 648 649 650 651 652 653 654 655 656 657 658 659 660 661 662 663 664 665 666 667 668 669 670 671 672 673 674 675 676 677 678 679 680 681 682 683 684 685 686 687 688 689 690 691 692 693 694 695 696 697 698 699 700 701 702 703 704 705 706 707 708 709 710 711 712 713 714 715 716 717 718 719 720 721 722 723 724 725 726 727 728 729 730 731 732 733 734 735 736 737 738 739 740 741 742 743 744 745 746 747 748 749 750 751 752 753 754 755 756 757 758 759 760 761 762 763 764 765 766 767 768 769 770 771 772 773 774 775 776 777 778 779 780 781 782 783 784 785 786 787 788 789 790 791 792 793 794 795 796 797 798 799 800 801 802 803 804 805 806 807 808 809 810 811 812 813 814 815 816 817 818 819 820 821 822 823 824 825 826 827 828 829 830 831 832 833 834 835 836 837 838 839 840 841 842 843 844 845 846 847 848 849 850 851 852 853 854 855 856 857 858 859 860 861 862 863 864 865 866 867 868 869 870 871 872 873 874 875 876 877 878 879 880 881 882 883 884 885 886 887 888 889 890 891 892 893 894 895 896 897 898 899 900 901 902 903 904 905 906 907 908 909 910 911 912 913 914 915 916 917 918 919 920 921 922 923 924 925 926 927 928 929 930 931 932 933 934 935 936 937 938 939 940 941 942 943 944 945 946 947 948 949 950 951 952 953 954 955 956 957 958 959 960 961 962 963 964 965 966 967 968 969 970 971 972 973 974 975 976 977 978 979 980 981 982 983 984 985 986 987 988 989 990 991 992 993 994 995 996 997 998 999 1000 1001 1002 1003 1004 1005 1006 1007 1008 1009 1010 1011 1012 1013 1014 1015 1016 1017 1018 1019 1020 1021 1022 1023 1024 1025 1026 1027 1028 1029 1030 1031 1032 1033 1034 1035 1036 1037 1038 1039 1040 104

181 CCTGGTGTCTGCCTCCTCCCCCTGGGCCCCAGGGTCCAGTATGG 240

b 115 cctgggtgtgcctcctccccctgccccaggcctggggccccccagggtccagtatgg 174

1312	agagctccaaacctgtagagaccagcagaggcttcggcagattccacctataattctg	13171
Qy	1441 TCATTGCTGTGTGGATAGAAACACAGCAGCAGATAGATCCCTATGTGGATCTCAGCT	15000
Db	1372 tcttgctggtgtgataagaacccaggacagtagatccctatgggttgatctcagct	14311
Qy	1501 GGAAGTTCGTTTGGAGCCCAATTCGTGTGAGACCCTGTATTTCAAAATTTGGAGCTGGAAG	15606
Db	1432 ggaagttctgtttgsggcctattctgtgagaccctgattttcaaatctgcagctgaaag	14911
Qy	1561 GTGCTGTGTACCTCTGATTTACCCCCAGAGCTTGGAGTTCGTCTCAAGGAACTGTGTATG	16200
Db	1492 gtgcttgtacctgtatttcacccagagtttgagttctgtcctcaaggaaacgtgtgtaatg	15511
Qy	1621 TGTACATCTGTGTCCATGTGTGACCATGTGTCTGTGAAG--CAGGGAACATGTATT-CTC	16777
Db	1552 tgtacatctctgtgcccatgtgtgaccatgtgtctgtggaagccagggaacatgtatctcttc	16111
Qy	1678 TGCATCATGTATGTAGTGCCCTGGGGAGTGTGTGTGGGTCCCTTGGCTTTTGGCTTTCC	17371
Db	1612 tgcatacatgtatgtagggtcgtcgtg--gagtggtgtgtggctctgctctgctggccctttcc	16688
Qy	1738 CATTGACGGGTGTGCAGGTGTGAATAAA 1767	
Db	1669 c--ttgcagggttgtgcaggtgtggaataa 1696	

AAA35197  
ID AAA35197 standard: DNA: 1696 BP.

DT 28-JUL-2000 (first entry)

Human; adenosine receptor; low adenosine antisense oligonucleotide; phosphorothioate; impaired respiration; inflammation; allergy; allergic disease; bronchoconstriction; inhibitor; antiinflammatory; antiasthmatic; cytotostatic; analgesic; impaired airway; lung disease; ischaemic condition; pulmonary vasoconstriction; asthma; respiratory distress syndrome; pain; cystic fibrosis; emphysema; pulmonary hypertension; chronic obstructive pulmonary disease; COPD; cancer; leukaemia; lymphoma; carcinoma; metastasis; ss.

XX  
PN WO200009525-A2.

PF 03-AUG-1999; 99WO-US17712.

PA . (UYEC-) UNIV EAST CAROLINA.

DR WPI; 2000-205971/18

PT New antisense oligonucleotides useful for treating e.g. pulmonary  
PT vasoconstriction, inflammation, allergies, asthma, hypertension,  
PT bronchitis, emphysema, respiratory distress syndrome, ischemia or  
PT cancers -

PS Disclosure: Page 1240: 1343pp: English.

CC The present invention describes a new composition comprising an  
CC antisense oligonucleotide (ON) with low adenosine (up to 15%), which  
CC targets nucleic acids involved in bronchoconstriction, allergies, and/or  
CC inflammation. The ON can have antiinflammatory, antiallergic,  
CC







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GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 3, 2001, 15:17:45 ; Search time 1394.56 Seconds  
(without alignments)  
12201.079 Million cell updates/sec

Title: US-09-532-263-4  
Perfect score: 1800  
Sequence: 1 TCTAACAGCCTTACCCCACT.....TTCTTGAGATTACTCTCAG 1800

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 10228115 seqs, 4726426750 residues

Total number of hits satisfying chosen parameters: 20456230

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

EST:\*

1:	gb_estl1:
2:	gb_est2:
3:	gb_est3:
4:	gb_est4:
5:	gb_est5:
6:	gb_est6:
7:	gb_est7:
8:	gb_est8:
9:	gb_est9:
10:	gb_est10:
11:	gb_est11:
12:	gb_est12:
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16:	gb_est16:
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25:	gb_est33:
26:	gb_est34:
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31:	gb_est39:
32:	gb_est40:
33:	em_estba:
34:	em_estfun:
35:	em_esthum1:
36:	em_esthum2:
37:	em_esthum3:
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42:	em_esthum8:
43:	em_esthum9:

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45:	em_esthum11:
46:	em_esthum12:
47:	em_esthum13:
48:	em_esthum14:
49:	em_esthum15:
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51:	em_esthum17:
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257: gb\_est188:\*  
258: gb\_est189:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.



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QY 1509 TGTGTTGGAGCCCATTTCTGTGAGACCCCTGTATTTCATAATTTGCAGCTGAAGAGTGCTTGT 1568
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Db 231 TGTGTTGGAGCCCATTTCTGTGAGACCCCTGTATTTCATAATTTGCAGCTGAAGAGTGCTTGT 172
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QY 1569 ACCTCTGATTTACCCAGAGTTGGAGTTCTGCTCAAGGAACGCTGTGTAATGTGTACATC 1628
|||||
Db 171 ACCTCTGATTTACCCAGAGTTGGAGTTCTGCTCAAGGAACGCTGTGTAATGTGTACATC 112
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QY 1629 TGTGTCATGTGTGACCATGTGTCTGTGAAGCAGGAACATGTAATCTCTCATGCAATGT 1688
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Db 111 TGTGTCATGTGTGACCATGTGTCTGTGAAGCAGGAACATGTAATCTCTCATGCAATGT 52
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QY 1689 ATGTAGTGTGCTGGGGAGTGTGTGGGTCTCTTGGCTTTGGCCCTTTCCCC 1739
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Db 51 ATGTAGTGTGCTGGGGAGTGTGTGGGTCTCTTGGCTTTGGCCCTTTATNCC 1

RESULT 2
AL525319 846 bp mRNA EST 13-FEB-2001
LOCUS AL525319 LTI_NFL003_NBC3 Homo sapiens cDNA clone CS0DC011YP14 5
DEFINITION Prime, mRNA sequence.
ACCESSION AL525319
VERSION AL525319.1 GI:12788812
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 846)
AUTHORS Li, W.B., Gruber, C., Jesses, J. and Polayes, D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.

FEATURES
Source 1..846
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="CS0DC011YP14"
/clone_lib="LTI_NFL003_NBC3"
/sex="male"
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/lab_host="DH10B"
/note="Organ: brain; Vector: pCMVSPORT 6; 1st strand cDNA
was primed with a NotI-oligo(dT) primer. Five prime end
enriched, double-stranded cDNA was digested with Not I and
cloned into the Not I and Eco RV sites of the pCMVSPORT 6
vector. Library was normalized. Library was constructed
by Life Technologies, Contact : Feng Liang Life
Technologies, a division of Invitrogen 9800 Medical Center
Drive Rockville, Maryland 20850, USA Fax : (1) 301 610
8371 Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com"

BASE COUNT 151 a 270 c 261 g 162 t 2 others
ORIGIN

Query Match 42.1%; Score 757.6; DB 105; Length 846;
Best Local Similarity 98.5%; Pred. No. 2.6e-182;
Matches 784; Conservative 2; Mismatches 6; Indels 4; Gaps 2;

QY 121 CCCACAGATGACGACGACGCTCTCAGGCGCTGAGCAGGCTCTGTGGCCGTGGCTACAGC 180
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Db 52 CACCGAGATGACGACGACGCTCTCAGGCGCTGAGCAGGCTCTGTGGCCGTGGCTACAGC 111
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QY 181 CTGTGTGTCTGCTCTCTCCCTGCCCCAGGCGCTGGGGCCCCCAGGGGTCCTCAGTATGG 240
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QY 301 CTGTTTCGGGATGGGAGGCAAAAGCTGCTCCAGGACCTGACTCTGGGCTAGGCGATGA 360
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Db 232 CTGTTTCGGGATGGGAGGCAAAAGCTGCTCCAGGACCTGACTCTGGGCTAGGCGATGA 291
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QY 361 ACTGCTCTTGCCCGCAGGACAGACAGCACTGATGAGGGACCTTACATCTGCCAGACCTTGA 420
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Db 292 ACTGCTCTTGCCCGCAGGACAGACAGCACTGATGAGGGACCTTACATCTGCCAGACCTTGA 351
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QY 421 TGTGTCACTTTGGGGGACAGTGACCCCTGACGTGGGTACCCCTCCAGCCGCCCTGTGTGT 480
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Db 352 TGTGTCACTTTGGGGGACAGTGACCCCTGACGTGGGTACCCCTCCAGCCGCCCTGTGTGT 411
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QY 481 CTCCTGCCAAGCAGCCGACTATGAGAACTCTCTTGACCTTGGAGTCCCAGCCAGATCAG 540
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QY 601 CCAGAGGAGGAGTCCATCCACAGGGCCCTGGCCATGCCACAGAGTCCCTTAGGGGCTGC 660
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Db 592 CCGCTGTGTTTCCACGGGCTGAGTCTTGAGCCAGTACCGGATTAATGTGACTGAGGT 651
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QY 721 GAACCCACTTGGGTGCTCCAGCACACGCTGCTGGATGTGAGCTTGACAGACATCTTTCG 780
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QY 781 CCCTGACCCACCCAGGCGCTGCGGGTAGAGTACAGTACAGGTTACCCCGAGGCGCTGC 840
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Db 709 CCCTGACCCACCCAGGCGCTGCGGGTAGAGTACAGTACAGGTTACCCCGAGGCGCTGC 768
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QY 841 AGCAGCTGGACATACCTGCTCTTGCCGCTGCCAGCCACCTCTCTGCTCAAGTTCCG 900
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Db 769 AGCAGCTGGACATACCTGCTCTTGCCGCTGCCAGCCACCTCTCTGCTCAAGTTCCG 827
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QY 901 TTTGCACTACCGTCCG 916
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Db 828 TTTGCACTACCGTCCG 843

RESULT 3
BF339055 833 bp mRNA EST 22-NOV-2000
LOCUS 602034848F1 NCI.CGAP_Brn64 Homo sapiens cDNA clone IMAGE:4183138
DEFINITION 5', mRNA sequence.
ACCESSION BF339055
VERSION BF339055.1 GI:11285475
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 833)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgaps-r@mail.nih.gov
Tissue Procurement: David N. Louis, M.D.
cDNA Library Preparation: Life Technologies, Inc.
DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
```

http://image.llnl.gov  
Plate: L1AM9498 row: o column: 11  
High quality sequence stop: 761.

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/organism="Homo sapiens"  
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/lab\_host="DH10B (T1 phage-resistant)"  
/note="Organ: Brain; Vector: pCMV-SPORT6; Site\_1: NotI;  
Site\_2: SalI; Cloned unidirectionally. Primer: Oligo dt.  
Average insert size 1.57 kb. Constructed by Life  
Technologies. Note: this is a NCI\_CGAP Library."

BASE COUNT 194 a 181 c 265 g 193 t  
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Query Match 38.2%; Score 687.8; DB 147; Length 833;  
Best Local Similarity 98.1%; Pred. No. 1.6e-164;  
Matches 717; Conservative 0; Mismatches 12; Indels 2; Gaps 2;

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QY 1125 CGCAGCCAGAGGTGGAGCCTCAGGTGGACAGCCTGCTCTCCAGGCGCTCCCTCCCAAC 1184  
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QY 1185 CACACCTCGGCTACTGTATCACAGGACCTGTGTGGAGCAGTACGTGTGCGGCTTT 1244  
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Db 121 CACACCTCGGCTACTGTATCACAGGACCTGTGTGGAGCAGTACGTGTGCGGCTTT 180  
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QY 1245 TGGGAATCCCTTTCTTCTGGGACTGTGTGGGCGCTGGGACTGGGCTGTGGCTGA 1304  
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Db 181 TGGGAATCCCTTTCTTCTGGGACTGTGTGGGCGCTGGGACTGGGCTGTGGCTGA 240  
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QY 1305 GGCTGAGACGGGTGGGAAGGTGATCCCAAGCCTGGGTCTTCTGGCCTCAGTGATTC 1364  
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Db 241 GGCTGAGACGGGTGGGAAGGTGATCCCAAGCCTGGGTCTTCTGGCCTCAGTGATTC 300  
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QY 1365 CAGTGGACAGCGTCCAGGAGCTCCAAACCTGTAGAGGACCCAGGAGGCTTGGCGAGAT 1424  
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QY 1425 TCCACCTATATCTGTCTGTGGTGTGATAGAACCCAGGAGGACAGTAGATCCCTA 1484  
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Db 361 TCCACCTATATCTGTCTGTGGTGTGATAGAACCCAGGAGGACAGTAGATCCCTA 420  
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QY 1485 TGGTTGGATCTCAGCTGGAAGTCTGTGTTGGAGCCCATTTCTGTGAGACCCCTGTATTCA 1544  
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Db 421 TGGTTGGATCTCAGCTGGAAGTCTGTGTTGGAGCCCATTTCTGTGAGACCCCTGTATTCA 480  
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Db 481 AATTGGCAGTGAAAGTGTGTGTACCTGTGATTTACCCAGAGTGGAGTTCGTGTCA 540  
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QY 1605 AGGAACCTGTGATGTATGTATCTGTCTCATGTGTGACCATGTGTCTGTGAAGCAGGG 1664  
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Db 541 AGGAACCTGTGATGTATGTATCTGTCTCATGTGTGACCATGTGTCTGTGAAGCAGGG 600  
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QY 1665 AACATGATTTCTCTGTCATGATGTATGTAGTGCTGGGAGTGTGTGGTCTTTGGC 1724  
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Db 601 AACATGATTTCTCTGTCATGATGTATGTAGTGCTGGGAGTGTGTGGTCTTTGGC 660  
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QY 1725 TCTTGGCCTTTCCCTTTCAGGGGTTGTGACGTTGTGAATAAGAGAATAAGGAAGTCT 1784  
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Db 661 TCTTGGCCTTT-CCTTTCAGGGGTTGTGACGTTGTGAATAAGAGAATAAGGAAGTCT 718  
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QY 1785 TGGAGATATTA 1795  
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Db 719 GGGACAAAAA 729

RESULT 4  
LOCUS AL580490/c 722 bp mRNA EST 16-FEB-2001  
DEFINITION AL580490 LTI\_NFL008\_TC2 Homo sapiens cDNA clone CS0DJ015YH07 3  
prime, mRNA sequence.  
ACCESSION AL580490  
VERSION AL580490.1 GI:12946563  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
Li, W.B., Gruber, C., Jessee, J. and Polayes, D.  
Full-length cDNA libraries and normalization  
Unpublished (2001)  
Contact: Genoscope  
Genoscope - Centre National de Sequencage  
BP 191 91006 EVRY cedex - France  
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.

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/clone="CS0DJ015YH07"  
/clone\_lib="LTI\_NFL008\_TC2"  
/sex="male"  
/tissue\_type="T cells from T cell leukemia"  
/note="Vector: pCMVSPORT 6; Site\_1: NotI; 1st strand cDNA  
was primed with a NotI-oligo(dT) primer. Five prime end  
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cloned into the Not I and Eco RV sites of the pCMVSPORT 6  
vector. Library was normalized. Library was constructed by  
Life Technologies. Contact : Feng Liang Life Technologies,  
a division of Invitrogen 9800 Medical Center Drive  
Rockville, Maryland 20850, USA Fax : (1) 301 610 8371  
Email : fliang@lifetech.com URL :  
http://fulllength.invitrogen.com"

BASE COUNT 171 a 223 c 170 g 142 t 16 others  
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Query Match 36.9%; Score 664.8; DB 106; Length 722;  
Best Local Similarity 95.0%; Pred. No. 1.1e-158;  
Matches 686; Conservative 14; Mismatches 10; Indels 12; Gaps 1;

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QY 1072 TCCGAGCAGCTGGGACCATACCAAGGAGATACAGCATGGGCGCAGCTACACAGCAGCC 1131  
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QY 1132 AGAGGTGGAGCTCAGGTGGAGACCCCTGCTCTCCAGGCGCTCCCTCCCAACACACCC 1191  
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Db 602 AGAGGTGGAGCTCAGGTGGAGACCCCTGCTCTCCAGGCGCTCCCTCCCAACACACCC 543  
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QY 1192 TCGGCTACTTGATCACAGGAGCTCTGTGGAGCAGTACGTGTGCTGGGCTCTTTGGGAAT 1251  
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Db 542 TCGGCTACTTGATCACAGGAGCTCTGTGGAGCAGTACGTGTGCTGGGCTCTTTGGGAAT 483  
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QY 1252 CCTTTCTTTCTCGGAGCTGGTGGCTGGGCGCTGGGCTGGGCTGGGCTGGGCTGGGCTGG 1311  
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Db 482 CCTTTCTTTCTCGGAGCTGGTGGCTGGGCGCTGGGCTGGGCTGGGCTGGGCTGGGCTGG 423  
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QY 1312 ACGGGCTGGGAGAGTGGATCCCAAGCCTGGGCTCTTTGGGCTCAGTGATTCAGTGGA 1371  
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Db 422 ACGGGCTGGGAGAGTGGATCCCAAGCCTGGGCTCTTTGGGCTCAGTGATTCAGTGGA 363  
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Db	160	TGTTGACCATCTGCTGTGAGCAGGAGAACATGATATCTCTGATGCATGATATGTAGGT	101
Qy	1697	GCCTGGGGAGTGTGTGGGGTCCCTTGGCTCTTGGCCCTTCCCTTGCAGGGGTTGTGCAG	1756
Db	100	GCCTGGGGAGTGTGTGGGGTCCCTTGGCTCTTGGCCCTTCCCTTGCAGGGGTTGTGCAG	41
Qy	1757	GTGTGAATAAGAGAATAAGGAAGTCTCTTGGAGATTATA	1795
Db	40	GTGTGAATAAGAGAATAAGGAAGTCTCTTGGAGATTATA	2
RESULT 7			
AW438628/c			
LOCUS	AW438628	611 bp	EST 14-FEB-2000
DEFINITION	x101c12.x1 NCI_CGAP_Ut4 Homo sapiens cDNA clone IMAGE:2777878 3' similar to TR:Q16542 Q16542 INTERLEUKIN-11 RECEPTOR. ;, mRNA sequence.		
ACCESSION	AW438628		
VERSION	AW438628.1		
KEYWORDS	EST.		
SOURCE	human.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
AUTHORS	1 (bases 1 to 611)		
TITLE	NCI-CGAP <a href="http://www.ncbi.nlm.nih.gov/ncicgap">http://www.ncbi.nlm.nih.gov/ncicgap</a> . National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index Unpublished (1997)		
JOURNAL	Contact: Robert Strausberg, Ph.D.		
COMMENT	Email: <a href="mailto:cgapbs-r@mail.nih.gov">cgapbs-r@mail.nih.gov</a> Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D. cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: Greg Lennon, Ph.D. DNA sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <a href="http://www-bio.llnl.gov/bbrp/image/image.html">www-bio.llnl.gov/bbrp/image/image.html</a> Seq primer: -40UP from Gibco High quality sequence stop: 391.		
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	/lab_host="DH10B"		
	/note="Organ: uterus; Vector: pcMV-SPORT6; Site_1: SalI; Site_2: NotI; Cloned unidirectionally. Primer: Oligo dt. Average insert size 1.48 kb. Life Technologies catalog #:		
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ORIGIN	172 a	195 c	124 g 120 t
Query Match 31.98; Score 573.6; DB 116; Length 611;			
Best Local Similarity 98.2%; Pred. No. 1.9e-135;			
Matches 601; Conservative 0; Mismatches 9; Indels 2; Gaps 2;			
Qy	1190	CCTCGGCTACTTATACACAGGACTCTGTGGAGCAGGTAGCTGTGCTGGCCTCTTTGGGA	1249
Db	611	CCTGGGTATTGATACAGGAGACTCTGTGGAGCAGGAGCTGTGCTGGCCTCTTTGGGA	552
Qy	1250	ATCCTTTCTTTTCCCT-GGGACTGTGGTGGGGCCCTGGCACTGGGGCTCTGGCTGAGGCT	1308
Db	551	ATCCTTTCTTTTCCCTGGGACATGGTGGTGGGGCCCTGGCACTGGGGTCTCGCTGAGGCT	492



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Qy 1309 GAGACGGGTGGGAGGATGATCCCAAGCCTGGGTTCTTGGCCCTCAGTGAATCCAGT 1368
Db 491 GAGACGGGTGGGAGGATGAT-CCCAAGCCTGGGTTCTTGGCCCTCAGTGAATCCAGT 433
Qy 1369 GGACAGGCGTCCAGAGCTCAAAACCTGTAGAGGACCCAGAGGGCTTCGGCAGATTCCA 1428
Db 432 GGACAGGCGTCCAGAGCTCAAAACCTGTAGAGGACCCAGAGGGCTTCGGCAGATTCCA 373
Qy 1429 CCTATAATCTCTGCTTGTGTGTGGATAGAAACCCAGCAGCAGACAGTAGATCCCTATGGT 1488
Db 372 CCTATAATCTCTGCTTGTGTGTGGATAGAAACCCAGCAGCAGACAGTAGATCCCTATGGT 313
Qy 1489 TGGATCTCAGCTGGAAGTCTCTTTGGAGCCCATTTCTGTGAGACCCCTGTATTTCAAATT 1548
Db 312 TGGATCTCAGCTGGAAGTCTCTTTGGAGCCCATTTCTGTGAGACCCCTGTATTTCAAATT 253
Qy 1549 TGCAGCTGAAAGTCTGTACCTCTGATTTACCCAGAGTTGGAGTTCGTCTCAAGGA 1608
Db 252 TGCAGCTGAAAGTCTGTACCTCTGATTTACCCAGAGTTGGAGTTCGTCTCAAGGA 193
Qy 1609 ACGTGTGAATGTGACATCTGTGTCATGTGTGACCATGTGTCTGTAAGCAGGGAACA 1668
Db 192 ACGTGTGAATGTGACATCTGTGTCATGTGTGACCATGTGTCTGTAAGCAGGGAACA 133
Qy 1659 TGTATCTCTGCATCATGTATGTAGTGGCCCTGGGAGTGTGTGGGTCTCTTGGCTCTT 1728
Db 132 TGTATCTCTGCATCATGTATGTAGTGGCCCTGGGAGTGTGTGGGTCTCTTGGCTCTT 73
Qy 1729 GGCCTTCCCTTCAGGGGTGTCAGGTGTGAATAAGAGAATAAGAAATCTTCTTGA 1788
Db 72 GGCCTTCCCTTCAGGGGTGTCAGGTGTGAATAAGAGAATAAGAAATCTTCTTGA 13
Qy 1789 GATTACTACG 1800
Db 12 GATTACTACG 1

RESULT 8
LOCUS BF435972/c
DEFINITION nab75h05.x1 Soares.NSF.F8.9W.OT.PA.P.S1 Homo sapiens CDNA clone IMAGE:3273825 3' similar to TR:Q16542 Q16542 INTERLEUKIN-11 RECEPTOR. ; mRNA sequence.
ACCESSION BF435972
VERSION BF435972.1 GI:11448287
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE 1 (bases 1 to 568)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -40UP from Gibco
High quality sequence stop: 439.
Location/Qualifiers
1. 568
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:3273825"
/lab_host="Soares.NSF.F8.9W.OT.PA.P.S1"
/note="Organ: pooled; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site:1: Not I; Site:2: Eco RI; Equal amounts of plasmid DNA from five normalized libraries were mixed, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in
```

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a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from pools of 5,000 clones made from the same 5 libraries. The pools consisted of the following libraries and clones: Soares Nhsf pool 1: 309384-310919, 323208-325895 Soares Nhsf pool 1: 145032-147335, 147720-148103, 148872-149255, 15002 - 150407, 151176-152327 Soares Nhsf pool 1: 758280-760583, 772104-774407 Soares Nhsf pool 1: 304776-306311, 320136-322823, 326280-326663 Soares Nhsf pool 1: 723720-726407, 739080-740999 Subtraction by Bento Soares and M. Fatima Bonaloo."
BASE COUNT 162 a 179 c 117 g 110 t
ORIGIN

Query Match 31.3%; Score 563.2; DB 148; Length 568;
Best Local Similarity 99.5%; Pred. No. 8.4e-133;
Matches 565; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1232 GTGCTGGCGTCTTTGGGAATCTTTTCTTCTGGGACCTGGTGGTGGGCGCCCTGGCACTG 1291
Db 568 GTGCTGGCGTCTTTGGGAATCTTTTCTTCTGGGACCTGGTGGTGGGCGCCCTGGCACTG 509
Qy 1292 GGGCTCTGGCTGAGCTGAGACGGGGTGGGAAGATGATCCCAAGCCTGGGTCTTGG 1351
Db 508 GGGCTCTGGCTGAGCTGAGACGGGGTGGGAAGATGATCCCAAGCCTGGGTCTTGG 449
Qy 1352 GCCTCAGTGAATCCAGTGCAGAGGCTCCAGAGCTCCAAACCTGTAGAGGACCCAGGAG 1411
Db 448 GCCTCAGTGAATCCAGTGCAGAGGCTCCAGAGCTCCAAACCTGTAGAGGACCCAGGAG 389
Qy 1412 GGCTTCGGCAGATCCACCTATAATCTTCTGCTGGTGGATAGAAACCCAGGAG 1471
Db 388 GGCTTCGGCAGATCCACCTATAATCTTCTGCTGGTGGATAGAAACCCAGGAG 329
Qy 1472 CAGTAGATCCCTATGGTGGATCTCAGCTGGAAGTCTGTTGGAGCCCATTTCTGTAG 1531
Db 328 CAGTAGATCCCTATGGTGGATCTCAGCTGGAAGTCTGTTGGAGCCCATTTCTGTAG 269
Qy 1532 ACCCTGTATTTCAAAATTTGCAGCTGAAAGGTCCTTGTACCTCTGATTTACCCCAAGATT 1591
Db 268 ACCCTGTATTTCAAAATTTGCAGCTGAAAGGTCCTTGTACCTCTGATTTACCCCAAGATT 209
Qy 1592 GGAGTCTCTCAAGGAACGCTGTGTAATGTGTACATCTGTGTCCATGTGTACCATGTGT 1651
Db 208 GGAGTCTCTCAAGGAACGCTGTGTAATGTGTACATCTGTGTCCATGTGTACCATGTGT 149
Qy 1652 CTGTGAACGAGGAACATGTATCTCTGCATGCATGTATGTAGTGCCTGGGAGTGTGT 1711
Db 148 CTGTGAACGAGGAACATGTATCTCTGCATGCATGTATGTAGTGCCTGGGAGTGTGT 89
Qy 1712 GTGGTCTCTTGGCTCTTGGCCCTTCCCTTTCAGGGGTTGTSCAGGTGTGAATAAGAGA 1771
Db 88 GTGGTCTCTTGGCTCTTGGCCCTTCCCTTTCAGGGGTTGTSCAGGTGTGAATAAGAGA 29
Qy 1772 ATAAGGAAGTCTTGGAGATTATATCTCA 1799
Db 28 ATAAGGAAGTCTTGGAGATTATATCTCA 1

RESULT 9
LOCUS BF434373
DEFINITION 7096c07.x1 NCI-CGAP.Ov18 Homo sapiens CDNA clone IMAGE:3644149 3' similar to TR:Q16542 Q16542 INTERLEUKIN-11 RECEPTOR. ; mRNA sequence.
ACCESSION BF434373
VERSION BF434373.1 GI:11446661
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
```



Db 132 CAGCGAGTCCGTGAAGCTGTGTTCTCTGGAGTGACTGCCGGGACCCAGCTGTCTCTGGT 191  
Qy 306 TTCGGATGGGAGCAAGCTGCTCCAGGACCTGACTCTGGGCTAGGGATGAACCTGG 365  
Db 192 TTCGGATGGGAGCAAGCTGCTCCAGGACCTGACTCTGGGCTAGGGATGAACCTGG 251  
Qy 366 TCCTGGCCAGGCAGACAGCACTGATGAGGCACTTACATCTGCCAGACCTGGATGGT 425  
Db 252 TCCTGGCCAGGCAGACAGCACTGATGAGGCACTTACATCTGCCAGACCTGGATGGT 311  
Qy 426 CACTTGGGGACAGTACCCTGGAGCTGGGCTACCTCCAGCCGCGCTGTGTCTCT 485  
Db 312 CACTTGGGGACAGTACCCTGGAGCTGGGCTACCTCCAGCCGCGCTGTGTCTCT 371  
Qy 486 GCAAGAGCCGCACTATGAGAACTTCTCTGACATGAGTCCAGCCAGATCAGCGGT 545  
Db 372 GCCAAGAGCCGCACTATGAGAACTTCTCTGACATGAGTCCAGCCAGATCAGCGGT 431  
Qy 546 TACCCAGCCGCTACCTCCTCCTACAGAAAGACAGTCTTAGAGCTGATGCCAGA 605  
Db 432 TACCCAGCCGCTACCTCCTCCTACAGAAAGACAGTCTTAGAGCTGATGCCAGA 491  
Qy 606 GGAGAGTCCATCCAGAGGCGCTGGCATGCCAGATCCCTAGGGCTGCCGCT 665  
Db 492 GGAGAGTCCATCCAGAGGCGCTGGCATGCCAGATCCCTAGGGCTGCCGCT 551  
Qy 666 GTGTTGTC 673  
Db 552 GTGTTGTC 559

RESULT 11  
BF434707  
LOCUS BF434707 514 bp mRNA EST 29-NOV-2000  
DEFINITION 7p03d01.x1 NCI-CGAP.Ov18 Homo sapiens cDNA clone IMAGE:3644593 3'  
similar to TR:Q16542 Q16542 INTERLEUKIN-11 RECEPTOR. ;, mRNA  
sequence.

ACCESSION BF434707  
VERSION BF434707.1 GI:11446995  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
Tumor Gene Index  
JOURNAL Unpublished (1997)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-remail.nih.gov  
Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael  
R. Emmert-Buck, M.D., Ph.D. cDNA Library Preparation: M. Bento  
Soares, Ph.D. cDNA Library Arrayed by: Christa Prange, The  
I.M.A.G.E. Consortium DNA Sequencing by: Washington University  
Genome Sequencing Center  
Clone distribution: NCI-CGAP clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL, send email to:  
info@image.llnl.gov  
Seq primer: -40UP from Gibco  
High quality sequence stop: 341.  
Location/Qualifiers  
1. 514  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="IMAGE:3644593"  
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/tissue\_type="fibrothoma"  
/lab\_host="DH10B (phage-resistant)"  
/note="Organ: ovary; Vector: pT73D-Pac (Pharmacia) with a  
modified polylinker; Site\_1: Not 1; Site\_2: Eco RI; 1st  
strand cDNA was primed with a Not I - oligo(dT) primer [5'  
TGTTACCAATCTGAAGTGGGAGCGCGCGCCGACATATTTTTTTTTTTTTT 3'];

double-stranded cDNA was ligated to Eco RI adaptors  
(Pharmacia), digested with Not I and cloned into the Not  
I and Eco RI sites of the modified pT73 vector. Library  
went through one round of normalization, and was  
constructed by Bento Soares and M. Fatima Bonaldo. "

BASE COUNT 93 a 166 c 152 g 97 t  
ORIGIN

Query Match 27.6%; Score 496.8; DB 148; Length 514;  
Best Local Similarity 97.5%; Pred. No. 6.9e-116;  
Matches 501; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

Qy 109 ACTCTACCTCTCCCCACAGATGAGCAGCAGCTGCTCAGGCTGAGCAGGGTCTCTGGTGGC 168  
Db 1 ACTCTACCTCTCCCCACAGATGAGCAGCAGCTGCTCAGGCTGAGCAGGGTCTCTGGTGGC 60  
Qy 169 CGTGCTACAGCCCTGTGTCTCTCTCCCTCCCGCCAGGCTGGGGCCCCCAGG 228  
Db 61 CGTGCTACAGCCCTGTGTCTCTCTCCCTCCCGCCAGGCTGGGGCCCCCAGG 120  
Qy 229 GTCCAGTATGGGACGAGCAGCTGCTGAAGCTGTGTTCTCTGGAGTGAATGCTGG 288  
Db 121 GGTCCAGTATGGGACGAGCAGCTGCTGAAGCTGTGTTCTCTGGAGTGAATGCTGG 180  
Qy 289 GGACCCAGTGTCTCTGGGATGGGAGCCAAAGCTGTCTCCAGGGACCTGACTCTGG 348  
Db 181 GGACCCAGTGTCTCTGGGATGGGAGCCAAAGCTGTCTCCAGGGACCTGACTCTGG 240  
Qy 349 GCTAGGGATGACCTGCTGGGACGAGCAGCAGCTGATGAGGACCTATCATCTG 408  
Db 241 GCTAGGGATGACCTGCTGGGACGAGCAGCAGCTGATGAGGACCTATCATCTG 300  
Qy 409 CCAGACCTGGATGTGCTGGGACGAGCAGCTGACCTGACCTGGGCTGAGCTCCAGC 468  
Db 301 CCAGACCTGGATGTGCTGGGACGAGCAGCTGACCTGACCTGGGCTGAGCTCCAGC 360  
Qy 469 CGGCCCTGTGTCTCTGCCAAGCAGCGACTATGAGAACTTCTCTTGGACCTTGGAGTCC 528  
Db 361 CGGCCCTGTGTCTCTGCCAAGCAGCGACTATGAGAACTTCTCTTGGACCTTGGAGTCC 420  
Qy 529 CAGCCAGATCAGCGGTGTACCCACCGCTACCTCCTCCTACAGGAGACACAGTCTCT 588  
Db 421 CAGCCAGATCAGCGGTGTACCCACCGCTACCTCCTCCTACAGGAGACACAGTCTCT 480  
Qy 589 AGGAGCTGATGCCAGAGGAGGAGTCCATCCACA 622  
Db 481 AGGAGCTGATGCCAGAGGAGGAGTCCATCCACA 514

RESULT 12  
AA454657/c  
LOCUS AA454657 502 bp mRNA EST 06-JUN-1997  
DEFINITION zx99g01.sl Soares\_NHMPu\_Sl Homo sapiens cDNA clone IMAGE:811920 3'  
similar to TR:G673438 G673438 CYTOKINE TYPE 1 RECEPTOR. ;, mRNA  
sequence.

ACCESSION AA454657  
VERSION AA454657.1 GI:2177433  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
AUTHORS 1 (bases 1 to 502)  
Kucaba,T., Lacy,M., Le.N., Lennon,G., Marra,M., Martin,J., Moore,B.,  
Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S.,  
Schellenberg,K., Steptoe,M., Tan,F., Theising,B., White,Y., Wyllie,  
T., Waterston,R. and Willson,R.  
WashU-Merck EST Project 1997  
Unpublished (1997)  
Contact: Wilson RK  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

RESULT	13
Ail149448/c	
LOCUS	Al149448 499 bp mRNA EST 28-OCT-1998
DEFINITION	cq72hl1.x1 Soares.placenta.8to9weeks.2nbhp8to9w Homo sapiens cDNA clone IMAGE:1715205 ; similar to TR/Q64385 Q64385 INTERLEUKIN 11 RECEPTOR, ALPHA CHAIN 2 PRECURSOR ; , mRNA sequence.
ACCESSION	Al149448
VERSION	Al149448.1 GI:3677917
KEYWORDS	EST.
SOURCE	human.
ORGANISM	Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS	1 (bases 1 to 499)
TITLE	NCI-CGAP <a href="http://www.ncbi.nlm.nih.gov/ncicgap">http://www.ncbi.nlm.nih.gov/ncicgap</a> . National Cancer Institute, Cancer Genome Anatomy Project (CGAP).
JOURNAL	Tumor Gene Index
COMMENT	Unpublished (1997) Contact: Robert Strausberg, Ph.D. Email: <a href="mailto:cgap@remail.nih.gov">cgap@remail.nih.gov</a> This clone is available royalty-free through LLNL ; contact the IMAGE Consortium ( <a href="mailto:info@image.llnl.gov">info@image.llnl.gov</a> ) for further information. Insert Length: 1724 Std Error: 0.00 Seq primer: -40m13 fwd. ET from Amersham High quality sequence stop: 459. Location/Qualifiers 1. .499
FEATURES	source

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/dev_stage=two placentae; one from 8 weeks and another
from 9 weeks post conception"
/lab_host="DH10B (ampicillin resistant)"
/note="Organ: Placenta; Vector: pT7T3D (Pharmacia) with a
modified polylinker; Site_1: Not 1; Site_2: Eco RI; 1st
strand cDNA was primed with a Not I - oligo(dT) primer [5'
TGTTACCAACTGTAAGTGGAGCGCGCGGATTTTTTTTTTTTTTTT 3'],
double-stranded cDNA was size selected, ligated to Eco RI
adapters (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of a modified pT7T3 vector
(Pharmacia). Library constructed by Bento Soares and
M. Patricia Bonaldo."
BASE COUNT      141 a      154 c      99 g      105 t
ORIGIN

Query Match      27.4%;      Score 492.6;      DB 16;      Length 499;
Best Local Similarity 99.2%;      Pred. No. 8e-115;
Matches 495;      Conservative 0;      Mismatches 4;      Indels 0;      Gaps 0;

Qy 1295 CTCGGCTGAGCGTGAAGCGGGTGGGAAGGATGGATCCCCAAAGCCGTGGGTCTCTGGCC 1354
Db 499 CTCGGCTGAGCGTGAAGCGGGTGGGAAGGATGGATCCCCAAAGCCGTGGGTCTCTGGCC 440
Qy 1355 TCAGTGATTCAGTGGACAGCGGCTCCAGAGCTCCAAACCTCTGACAGGACCCAGAGGGC 1414
Db 439 TCAGTGATTCAGTGGACAGCGGCTCCAGAGCTCCAAACCTGTGAGGACCCAGAGGGC 380
Qy 1415 TTCGCGAGATCCACCTATAATCCTGTCTGCTGGTGTGGATAGAAACACGACGACAC 1474
Db 379 TTCGCGAGATCCACCTATAATCCTGTCTGCTGGTGTGGATAGAAACACGACGACAC 320
Qy 1475 TAGATCCCTATGGTGGATCTCAGCTGAAGTCTGTTTGGAGCCCATTTCTGTGAGACC 1534
Db 319 TAGATCCCTATGGTGGATCTCAGCTGAAGTCTGTTTGGAGCCCATTTCTGTGAGACC 260
Qy 1535 CTGTATTTCAAATTGACAGCTGAAAGGTGCTGTACCTCTGTATTTTCACCCACAGTTGA 1594
Db 259 CTGTATTTCAAATTGACAGCTGAAAGGTGCTGTACCTCTGTATTTTCACCCACAGTTGA 200
Qy 1595 GTTCGTGTCGAAGGACGTGTGTAATGTGTACATCTGTGTCCATGTGTGACCATGTGTCTG 1654

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Db 199 GTTCTGCTCAAGGAACGTGTGTAAATGTGTACATCTCTGTGCCCATGTGTGACCATGTGTCTG 140

QY 1655 TGAAGCAGGGAACATGATTCTCTGCATGCATGATATAGTGCCCTGGGAGTGTGTGTG 1714  
|||||  
Db 139 TGAGGCAGGGAACATGATTCTCTGCATGCATGATATAGTGCCCTGGGAGTGTGTGTG 80  
|||

QY 1715 GGTCTTTGGCTCTTTGGCCTTTCCCCTTCAGCGGGTGTGCAGGTGTGAATAAAGAAGAATA 1774  
|||||  
Db 79 GGTCTTTGGCTCTTTGGCCTTTCCCCTTCAGCGGGTGTGCAGGTGTGAATAAAGAAGAATA 20  
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QY 1775 AGGAAGTCTTGGAGATTA 1793  
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Db 19 AGGAAGTCTTGGAGATTA 1  
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RESULT 14

BG537915

LOCUS BG537915 1067 bp mRNA EST 03-APR-2001

DEFINITION 602565788F1 NIH\_MGC\_77 Homo sapiens cDNA clone IMAGE:4690436 5',  
mRNA sequence.

ACCESSION BG537915

VERSION BG537915.1 GI:13530147

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 1067)  
NIH-MGC http://mgc.nci.nih.gov/.  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
Contact: Robert Strausberg, Ph.D.  
Email: cgapbs@mail.nih.gov

REFERENCE Tissue Procurement: CLONTECH Laboratories, Inc.  
CDNA Library Preparation: CLONTECH Laboratories, Inc.  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>

PLATE L1CM1507 row: p column: 21

HIGH QUALITY sequence stop: 590.

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/lab\_host="DH10B (T1 phage-resistant)"  
note="Organ: lung; Vector: pDNR-LIB (Clontech); Site: 1;  
SfiI (ggccattatgcc); Site: 2; SfiI (ggccattatgcc); 5' adaptor  
3' adaptors were used in cloning as follows: 5' adaptor  
sequence: 5'-CACGCCATTATGCC-3' and 3' adaptor sequence:  
5'-ATTCTAGAGCCAGGCGGCAGATC-dt(30)BN-3' (where B = A,  
C, or G and N = A, C, G, or T). Average insert size 1.  
kb (range 0.5-4.0 kb). 12/15 colonies contained inserts  
by PCR. This library was enriched for full-length clones  
and was constructed by Clontech Laboratories (Palo Alto,  
CA). Note: this is a NIH\_MGC Library."  
BASE COUNT 232 a 302 c 361 g 172 t  
ORIGIN

Query Match 27.1%; Score 488; DB 155; Length 1067;  
. Best Local Similarity 83.7%; Pred. No. 1.5e-113;  
Matches 748; Conservative 0; Mismatches 115; Indels 31; Gaps 1

QY 580 GACAGTCCTTAGGAGCTGATAGCCAGAGGAGGAGTCCATCCACAGGCCCTTGGCCATGCC 639  
|||||

Db 1 GACAGTCCTTAGGAGCTGATAGCCAGAGGAGGAGTCCATCCACAGGCCCTTGGCCATGCC 60  
|||||

QY 640 ACAGGATCCCTTAGGGGCTGCCCGCTGTGTGTFTCCACGGGGCTGAGTCTTGAGCCAGTA 699  
|||||

Db	61	ACAGATCCCCCTAGGGGCTG--CCGGCTGTGTGTCCACGGGGCTGAGTTCTTGGAGCAGTA	119
Qy	700	CCGATTAACTGACTGAGGTGAACCCACTGGGTGGTCCAGCACACGCCCTGCTGGAATGT	759
Db	120	CCGATTAACTGACTGAGGTGAACCCACTG---GGTCCAGCACACGCCCTGCTGGAATGT	176
Qy	760	GAGCTTGCGAGAGCATTTTGCGCCCTGACCCACCCAGGCCCTGCGGGTAGAGTCA-GTAC	818
Db	177	GAGCTTGCGAGAGCATTTTGCGCCCTGAGCCACCC--AGGCCCTGCGGGTAGAGTCAAGTAC	234
Qy	819	CAGTTACCCCGGAGGCTTGCAGGCCACTGGACATACCTTGCCTCTGCGCGTGCACAGC	878
Db	235	CAGTTACCCCGGAGGCTTGCAGGCCACTGGACATACCTTGCCTCTGCGCGTGCACAGC	294
Qy	879	CCCACTTCTCTCAAGTTCCGTTTGGACGTCGTCGGCGCAGC-ATCCAGCCTGTGCC	937
Db	295	CCCACTTCTCTCAAGTTCCGTTTGGACGTCGTCGGCGCAGC-ATCCAGCCTGTGCC	354
Qy	938	ACGTTGGAGCCAGCTGGACTGGAGAGGTGATCACAGATGCTGTGGCTGGGCTGCCCAT	997
Db	355	ACGTTGGAGCCAGCTGGACTGGAGAGGTGATCACAGATGCTGTGGCTGGGCTGCCCAT	414
Qy	998	GCTGTACAGTCACTGTCGCCGGACTTTCTAGATGCTGGCAGCTGTGGAGCACCTGGAGCCCG	1057
Db	415	GCTGTACAGTCACTGTCGCCGGACTTTCTAGATGCTGGCAGCTGTGGAGCA-CTTGAAGCC	473
Qy	1058	GAGCCCTGGGAACTCCGAGCAGCTGGGACCATACCAAGAGAGATACACAGCATGGGCCAG	1117
Db	474	GAGCCCTGGGAACTCCGAGCAGCTGGGACCATACCAAGAGAGATACACAGCATGGGCCAG	532
Qy	1118	CTACACGCGACGAGGTGGAGCCTCAGCTGGACAGCCCTGCTTCCCTCAAGGCCCTGCC	1177
Db	533	CTAACAGCCAG-CAGAGGTGGAG-CTCAGGTGGACGCC--TGTCTCCAGGCC----	584
Qy	1178	CTCAACACACACCTCTGGCTACTTGTATCACAGGAGCTCTGTGGAGCAGGTAGC---TGTG	1234
Db	585	--TCTCAACAGAGCTCGGTACTTGTATCCAGGAGACTCTGTGGACCCAGCTACTTGTGG	642
Qy	1235	CTGGCGCTTTGGGAATCCTTTCTTCTCTGGAC--TGTGGCTGGGCGCTGGCACTGGG	1293
Db	643	TGGCGACTTGGCAAAATCTTCTTCTCTGGAGCTTGTGGGTGTGGCCCTGGACTGGG	702
Qy	1294	G--CTCTGGCTGAGGCTGAGAGCGGTGGGAAGATGATGATCCCAAGGCCCTGGTCTGTG	1351
Db	703	GGCTCGGTGAGGCTGCACCTCGCGGTGGCAAGATGGTCCCCAAGCGGGTCTTGTGT	762
Qy	1352	GCCTCAGTGATTCAGTGGAGCGGCTCCAGAGCTCCAAACCTGTAGAGACCCAGAG	1411
Db	763	GCC---AGTAGTTCACTGGCCAGGGTCCAAAG--GCCAACCGGTACGAGCCAGGAG	817
Qy	1412	GGCTTCGGCAGATCCACCTATATCTCTTCTGTGTGTGGATAGAAACAG	1465
Db	818	GGTCTCGCAAGACCCCAATAAATGGCCGAGTGGGGTGGGGAACCCCG	871
RESULT 15			
AA456272			
LOCUS	AA456272	528 bp	EST
DEFINITION	z99901.r1 Soares_NHMPU.S1 Homo sapiens cDNA clone IMAGE:811920 5'		
	Similar to TR:G999450 G999450 INCOMPLETE INTERLEUKIN-11 RECEPTOR		
	ISOFORM ; mRNA sequence.		
ACCESSION	AA456272		
VERSION	AA456272.1		
KEYWORDS	EST.		
SOURCE	human.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
	1 (bases 1 to 528)		
	Hillier, L., Allen, M., Bowles, L., Dubuque, T., Geisel, G., Jost, S.,		
	Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M., Martin, J., Moore, B.,		
	Schellenberg, K., Steptoe, M., Tan, F., Theising, B., White, Y., Wyllie,		
	T., Waterston, R. and Willson, R.		

TITLE  
JOURNAL  
COMMENT

WashU-Merck EST Project 1997  
Unpublished (1997)  
Contact: Wilson RK  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: est@watson.wustl.edu  
This clone is available royalty-free through LNL; contact the  
IMAGE Consortium (info@image.llnl.gov) for further information.  
Seq primer: -28ml3 rev2 Ef from AmerSham  
High quality sequence stop: 504.  
Location/Qualifiers  
1. 528

FEATURES

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(Pharmacia) with a modified polylinker; Site\_1: Not I;  
Site\_2: Eco RI; Equal amounts of plasmid DNA from three  
normalized libraries (melanocyte 2NbHM, pregnant uterus  
NbHPU, and fetal heart NbHH19W) were mixed, and ss circles  
were made in vitro. Following HAP purification, this DNA  
was used as tracer in a subtractive hybridization  
reaction. The driver was PCR-amplified cDNAs from pools of  
5,000 clones made from the same 3 libraries. The pools  
consisted of I.M.A.G.E. clones 260232-265223,  
340488-345479, and 484488-489479."  
98 a 176 c 157 g 97 t

BASE COUNT  
ORIGIN

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Best Local Similarity 99.0%; Pred. No. 3.6e-110;  
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DB 128 TACCCTGCTCTCTGCGCGTGG - CAGGCCCACTTCCCTGCTCAAGTTCGTTTGCAGTACCGT 186  
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GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 3, 2001, 16:08:36 ; Search time 2420.96 Seconds  
(without alignments)  
11500.375 Million cell updates/sec

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Perfect score: 1800  
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Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 1344157 seqs, 7733874588 residues

Total number of hits satisfying chosen parameters: 2688314

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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97: gb\_pr10:\*  
98: em\_ba3:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

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3	1549.2	86.1	1696	97	HSU32324
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					U32324 Human inter
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					AF347936 Rattus no
					U14412 Mus musculus
					X74953 M.musculus
					X98519 M.musculus



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 VERSION 238102.1 GI:995653  
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 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
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 AUTHORS Cherel M., Sorel M., Lebeau B., Dubois S., Moreau J.F.,  
 Bataillie R., Minvielle S. and Jacques Y.  
 TITLE Molecular cloning of two isoforms of a receptor for the human  
 hematopoietic cytokine interleukin-11  
 JOURNAL Blood 86 (7), 2534-2540 (1995)  
 MEDLINE 95399754  
 REFERENCE 2 (bases 1 to 1682)  
 AUTHORS Cherel M.  
 TITLE Direct Submission  
 JOURNAL Submitted (13-OCT-1994) Michel Cherel, Institut de biologie, INSERM  
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polyA\_signal

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## RESULT 3

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ACCESSION U32324  
VERSION U32324.1 GI:975336  
KEYWORDS  
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ORGANISM Homo sapiens  
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Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 (bases 1 to 1696)  
AUTHORS Van Leuven, F., Stas, L., Hilliker, C., Miyake, Y., Bilinski, P. and Gossler, A.  
TITLE Molecular cloning and characterization of the human interleukin-11 receptor alpha-chain gene, IL11RA, located on chromosome 9p13  
JOURNAL Genomics 31 (1), 65-70 (1996)  
MEDLINE 96404003  
REFERENCE 2 (bases 1 to 1696)  
AUTHORS Van Leuven, F.  
TITLE Direct Submission  
JOURNAL Submitted (26-JUL-1995) Human Genetics, K.U.Leuven, Campus Gasthuisberg ON06, Leuven, Belgium, B-3000

## FEATURES

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QY 734 GTGTCAGACACAGCTGCTGTGATGTGAGTGTGACAGAGTCTTGGCCCTGACCCACC 793
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RESULT 5
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LOCUS Rattus norvegicus interleukin 11 receptor alpha chain precursor,
DEFINITION mRNA, complete cds.
ACCESSION AF347936
VERSION AF347936.1 GI:13549074
KEYWORDS Norway rat.
SOURCE Rattus norvegicus
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
REFERENCE 1 (bases 1 to 1713)
AUTHORS Li,R., Hartley,L. and Robb,L.
TITLE Expression of interleukin-11 and interleukin-11 receptor alpha
chain in the rat uterus in the peri-implantation period
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1713)
AUTHORS Robb,L. and Li,R.
TITLE Direct Submission
JOURNAL Submitted (08-FEB-2001) Cancer and Haematology Division, The Walter
and Eliza Hall Institute of Medical Research, PO Royal Melbourne
Hospital, Vic 3050, Australia
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BASE COUNT 324 a 473 c 548 g 368 t  
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Query Match 54.6%; Score 982.6; DB 94; Length 1713;  
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DB 1132 ATCAGAGGAGCCCTTGGAGCAAGTGGCTGTGTAGCAATCTCTGGGAATCTTCTTCTTTC 1191  
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DB 1604 CG--TTCTCGTGTGTGTGTATAGATGATGAGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1661  
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RESULT 6

MMU14412 1681 bp mRNA ROD 28-NOV-1994  
LOCUS Mus musculus interleukin-11 receptor alpha-chain mRNA, complete cds.  
DEFINITION  
ACCESSION U14412  
VERSION U14412.1 GI:576454  
KEYWORDS  
SOURCE house mouse.  
ORGANISM Mus musculus  
REFERENCE 1 (bases 1 to 1681)  
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
TITLE Cloning of a murine il-11 receptor alpha-chain; requirement for gp130 for high affinity binding and signal transduction  
JOURNAL EMBO J. 13, 4765-4775 (1994)  
MEDLINE 95045367  
REFERENCE 2 (bases 1 to 1681)  
AUTHORS Hilton,D.J.  
TITLE Direct Submission

JOURNAL	Submitted (07-SEP-1994)	Douglas J. Hilton, The Walter and Eliza Hall Institute of Medical Research, Royal Parade, Parkville, Victoria 3050, Australia
FEATURES	Location/Qualifiers	
source	1. .1681	
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QY	692 AGCCAGTACCGGATTAATGTGACTGAGGTGAACCCACTGGGTGTGTCAGCACAGCGCTG	751
DB	609 AGTGAGTACCGGATCAATGTGACCGAGGTGAACCACTG---GGTGGCAGCAGCTGGCTA	665









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Db	778	GAGGAAAGT	CCATCCAC	CGGCGCTT	GGCCGTGT	CCACAGGACCTC	TGGAGGCG	CTCCG	837
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Qy	964	GGTGATC	ACAGATG	CTGTG	GTGGTGC	CCCCATG	CTGTAC	GAGTGC	1023
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Qy	1725	TCTTGGCCTTTCCCTTGCAGGGGTTTGTGCAGGTGTGAATTAAGAGAATAAGGAAGTTCT	1784
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Db	1952	GGAAAAAANA	1962
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DEFINITION	Sequence 3 from Patent WO95959608.		PAT
ACCESSION	AX010400		
VERSION	AX010400.1	GI:9997251	
KEYWORDS			
SOURCE	Murinae gen. sp.		
ORGANISM	Murinae gen. sp.		
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostom		
	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae.		
REFERENCE	1 (bases 1 to 1140)		
AUTHORS	Austin, R.C. and Shaughnessy, S.		
TITLE	Osteoporosis treatment		
JOURNAL	Patent: WO 95959608-A 3 25-NOV-1999;		
	HAMILTON CIVIC HOSPITAL RESEAR (CA)		
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Qy	128	ATGAGCAGCAGCTGCTCAGGGCTGAGCAGGGTCCCTGGTGGCCGTGGCTACAGCCCTGGTG	187	
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Db	61	TCTTCTCTCTCCCTTGCCCTGCCCCAAGCTTGGGGTCTCCAGGGTCCAGTATGGACAACCT	120	
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Qy	308	CGGGATGGGGAGCCAAAGCTGTCTCAGGAGACCTGACTCTGGGCTAGGCGATGAACCTGGTC	367	
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Qy	368	TTGGCCCCAGGCAGACAGCACTGATGAGGGCACCTACATCTGCCAGACCCCTGGATGGTGCA	427	
Db	241	TTGGCCCCAGGTGGACAGGCCCTGATGAAGGCACTTATGTCTGCCAGACCCCTGGATGGTGTA	300	
Qy	428	CTTGGGGCAGACTGACCTTCGAGCTGGGCTACCCCTCCAGCCCGCCCTGTTGTCTCTCTGC	487	
Db	301	TCAGGGGGCATGGTGACCTCGAAGCTGGGCTTTCCCCACAGACGTCCTGAAGTCTCTCTGC	360	
Qy	488	CAAGCAGCCGACTATGAGAACTTCTCTTGCACCTGGAGTGCCAGGCAGATCAGCGGGTTTA	547	
Db	361	CAAGCGGTAGACTATGAAAACTTCCTCTGTAATCTGGAGTCCAGGCCAGGTACCGGGTTTG	420	







